

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2006, 08:31:33 ; Search time 4611.99 Seconds
(without alignments)
10611.945 Million cell updates/sec

Title: US-09-934-249-3

Perfect score: 861
Sequence: 1 atgcacccgttgatg9999gt.....aacagaaagacacccttc 861

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: gb_ba:*
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4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	861	100.0	861	6 AX392419	AX392419 Sequence
2	861	100.0	1321	6 AX392417	AX392417 Sequence
3	861	100.0	4519	6 CO894692	CO894692 Sequence
4	861	100.0	4839	6 CO812357	CO812357 Sequence
5	861	100.0	4839	6 CO896247	CO896247 Sequence
6	861	100.0	4839	6 CO976475	CO976475 Sequence
7	861	100.0	4839	6 CO981430	CO981430 Sequence
8	861	100.0	4839	6 AF305616	AF305616 Sequence
9	861	100.0	4930	6 CS130796	CS130796 Sequence
10	859.4	99.8	1383	6 AX775889	AX775889 Sequence
11	859.4	97.5	1061	8 BC015918	BC015918 Homo sapi
12	755.2	87.7	969	6 BD272494	BD272494 Secreted
13	754.2	87.6	1141	8 AF224278	AF224278 Homo sapi
14	754.2	87.6	4538	6 CS130841	CS130841 Sequence
15	753.8	87.5	1913	6 BD272544	BD272544 Secreted
16	753.6	87.5	969	6 BD272514	BD272514 Secreted
17	753.6	87.5	969	6 BD272515	BD272515 Secreted
18	753.6	87.5	969	6 BD272516	BD272516 Secreted

19	753.6	87.5	1140	6 AR336830	AR336830 Sequence
20	752.8	87.4	759	6 AR336831	AR336831 Sequence
21	752.6	87.4	1085	6 AX775887	AX775887 Sequence
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23	752	87.3	1818	8 AY128643	AY128643 Homo sapi
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25	751.2	87.2	756	6 BD272495	BD272495 Secreted
26	750.4	87.2	1060	6 BD272534	BD272534 Secreted
27	749.4	87.0	1630	8 BC080635	BC080635 Homo sapi
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ALIGNMENTS

RESULT 1	AX392419	861 bp	DNA	linear	PAT 23-MAR-2002
LOCUS	AX392419				
DEFINITION	Sequence 3 from Patent WO0216416.				
ACCESSION	AX392419				
VERSION	AX392419.1	GI:19700734			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE	Lee,R.T., Landeschulz,K.T., Kennedy,S.P., Thompson,J.F. and Turi,T.G.				
AUTHORS					
TITLE	Diagnosis and treatment of cardiovascular conditions				
JOURNAL	Patent: WO 0216416-A 3 28-FEB-2002;				
FEATURES	THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; PFIZER INC. (US)				
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ORIGIN					
Query Match	100.0%;	Score 861;	DB 6;	Length 861;	
Best Local Similarity	100.0%;	Pred. No. 1.4e-126;			
Matches	861;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1 ATGCACCGCTTGAATGGGGGTCAACAGCAGCCGCGCGCGCGCGCGGAGCCCAATGTC	60			

[illegible]

FEATURES	source	location/Qualifiers
ALPHORS	Lee,R.T., Landeschulz,K.T., Kennedy,S.P., Thompson,J.F. and Thri,T.G.	
TITLE	Diagnosis and treatment of cardiovascular conditions	
JOURNAL	Patent: WO 0216416-A 1 28-FEB-2002;	
	THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; PFIZER INC. (US)	
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ORIGIN		
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Best Local Similarity	100.0%; Pred. No. 1,3e-126;	
Matches	861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 ATGCACCGCTTGATGGGAGGTCAACAGACACCGCGCGCGCGCGCGGAGCCCAATGTC	60
DB	413 ATGCACCGCTTGATGGGAGGTCAACAGACACCGCGCGCGCGCGGAGCCCAATGTC	472
QY	61 TCCGCAACGCGCACTGCAGAAAGCTCTTGTTCAGAGCATGAGATCAGGAGCTGGAG	120
DB	473 TCCGCAACGCGCACTGCAGAAAGCTCTTGTTCAGAGCATGAGATCAGGAGCTGGAG	532
QY	121 TTGTTCAGATCATCATCATCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG	180
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DB	773 GTGCGCGCTTTCGCGCAGCGGAGCGCTTCACACGCTTTCAGCCCACTTATCGTCACTG	832
QY	421 CAGCAGAGATGCACTGTCCACCCACCAACCATCTTCGTGTCAAGCGGAGAGAGAGAGAGAG	480
DB	833 CAGCAGAGATGCACTGTCCACCCACCAACCATCTTCGTGTCAAGCGGAGAGAGAGAGAGAG	892
QY	481 TACCAAGGCGCTTCGACACCTTCAGCTTCGGAGACCCCGAGCAGAGCTGGAACTGAACCG	540
DB	893 TACCAAGGCGCTTCGACACCTTCAGCTTCGGAGACCCCGAGCAGAGCTGGAACTGAACCG	952
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DB	953 GAGTCGAGCGCAGACCCCGAAGAGACATCTTTCGACAGTGAACCTGATGATGATGTC	1012
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DB	1013 AGGCTGGGCGGCGCGCTGCGCGCGCGCGCGCGAGCATTCGAGCGCATCAGCGCCAGTGTCTAC	1072
QY	661 AGGCGCGGCGCATGAGAGGCGCGCGCGCGCGCATCAGCGCGAGTTCATCGGCACCTACCG	720

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Db	1133	GGGTCTCTCTCTTCAGCACCAGCAGAGCATGTGGGCGCCCTCTCTTGTGTGAGGGAGCCCGG	1192
Qy	781	CTCCACCCACACACATCGCGCGCCCTTAGAAGCGCGGCGCATCTGGAGCAAGAAGAGAT	840
Db	1193	CTCCACCCACACACATCGCGCGCCCTTAGAAGCGCGGCGCATCTGGAGCAAGAAGAGAT	1253
Qy	841	AAACAGAAAGACACCTCTTC	861
Db	1253	AAACAGAAAGACACCTCTTC	1273
RESULT 3			
CO894692			
LOCUS	CO894692	4519 bp	DNA
DEFINITION	CO894692	2 from Patent EP1471075.	linear
ACCESSION	CO894692		
VERSION	CO894692.1	GI:55467441	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
Source			
ORIGIN			
Query Match	100.0%;	Score 861;	DB 6;
Best Local Similarity	100.0%;	Pred. No. 1.1e-126;	Length 4519;
Matches	861;	Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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Qy	61	TCCTGCACGTGCAACTGCAAAAGCGCTTTTGTTCAGAGCATGAGATCACGAGGCTGGAG	120
Db	61	TCCTGCACGTGCAACTGCAAAAGCGCTTTTGTTCAGAGCATGAGATCACGAGGCTGGAG	120
Qy	121	TTTGTTCAGATCATCATCATCTGTTGGTGGTGAATGATGATGATGATGATCATCATCTGC	180
Db	121	TTTGTTCAGATCATCATCATCTGTTGGTGGTGAATGATGATGATGATGATGATCATCATCTGC	180
Qy	181	CTGCTGAGGCACTTACAGCTGTCTGACAGGTCCTTCATGAGCGGACAGCCAGAGGGAGCGG	240
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Qy	241	AGGAGAGAGATGACCTGTCTCTCAGAAAGATGCTGTGGCCCTCGAGAGACAAGTGTCA	300
Db	241	AGGAGAGAGATGACCTGTCTCTCAGAAAGATGCTGTGGCCCTCGAGAGACAAGTGTCA	300
Qy	301	GGCAACGAGATCCACAGGCGGAGCTTACGCGCCGCTCGGCCACCGACCGCTGGCC	360
Db	301	GGCAACGAGATCCACAGGCGGAGCTTACGCGCCGCTCGGCCACCGACCGCTGGCC	360
Qy	361	GTGCGGCGCTTGGCGGCGGAGGGAGGCGCTTCAACCGTTTCAGCGCCACCTATCGTACCTG	420
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Qy	421	CAGACGAGATTCGACCTGCGACCCACCATTCTCGCTGTCAACGCGGGAGAGACCCCAACC	480
Db	421	CAGCAGCAGATTCGACTCTGCGACCCACCATCTCGGTGTCAAGCGGGAGAGACCCCAACC	480
Qy	481	TACCAAGGAGCCCTTGACCTTCAGCTTCGGGACCCCGAGCAGAGCTTGAACTGAAACCCG	540
Db	481	TACCAAGGAGCCCTTGACCTTCAGCTTCGGGACCCCGAGCAGAGCTTGAACTGAAACCCG	540
Qy	541	GAGTCGGTGGCGGACCCCAACAGAACCATCTTGACAGTGCACGATGGATAGTGCC	600
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Qy	661	AGCGCGGAGCGCATGAGGAGGCGCGCGCCACCTACAGCGAGGTCAATCGCTACCTACCCG	720
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Qy	781	CTCCACGACACACATCGCGGCCCTTGAAGAGCGCAGCATCTTGAGCAAGAGAGAT	840
Db	781	CTCCACGACACACATCGCGGCCCTTGAAGAGCGCAGCATCTTGAGCAAGAGAGAT	840
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RESULT 4			
LOCUS	COB12357	4839 bp	DNA
DEFINITION	Sequence 109 from Patent WO2004038020.	linear	PAT 24-MAY-2004
ACCESSION	COB12357		
VERSION	COB12357.1	GI:47601977	
KEYWORDS			
SOURCE			
ORGANISM			
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	Hominidae; Homo.		
REFERENCE			
AUTHORS	Wittig,R., Poustka,A., Mollenhauer,J. and Schendendorf,D.		
TITLE	Target genes for the diagnosis and treatment of cancer		
JOURNAL	Patent: WO 2004038020-A 109 06-MAY-2004;		
	Deutsches Krebsforschungszentrum Stiftung des oeffentlichen n Rechte		
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Db	321	ATGACACGGCTTGATGGGGGTCAACGACGACCGCGCGCGCGCGCGAGCCCAATGTC	380
Qy	61	TCTGCAAGTGCACATGCAAAAGCTCTTTGTTCCAGAGCATGAGATCAGAGAGTGGAG	120
Db	381	TCTGCAAGTGCACATGCAAAAGCTCTTTGTTCCAGAGCATGAGATCAGAGAGTGGAG	440

Qy	422	CAGACACGAGATCGACTGCGACCCACCATCTGCGTGCAGCGGGAGAGAGCCCCCACC	480
Db	741	CAGACGAGATCGACTGCGACCCACCATCTCTGCTGCAGCGGGAGAGAGCCCCCACC	800
Qy	481	TACCAAGAGCCCTTGCACCCCTTCAGCTTTCGGGACCCCGAGCGAGCTTGAATGAACCG	540
Db	801	TACCAAGAGCCCTTGCACCCCTTCAGCTTTCGGGACCCCGAGCGAGCTTGAATGAACCG	860
Qy	541	GAGTCGGTGGCGCGACCCCGCAAGAAACATCTTTCGACAGTGAACCTGATGATGAGGC	600
Db	861	GAGTCGGTGGCGCGACCCCGCAAGAAACATCTTTCGACAGTGAACCTGATGATGAGGC	920
Qy	601	AGGCTGGCGGCCCCCTGCGCCCCCGACGAGTAATCTCGGCGATCAGCGCCACGTGTACGGC	660
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Qy	661	AGCGCGGGCGCATGAGAGGGGCGCGCGCCACTACAGCGAGGTTCATGTGGCACTAACCG	720
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Qy	721	GAGTCTCTCTTCAGCACGACGAGAGAGTGGGCGCGCTCTCTTGTCTGAGGGGACCGG	780
Db	1041	GAGTCTCTCTTCAGCACGACGAGAGAGTGGGCGCGCTCTCTTGTCTGAGGGGACCGG	1100
Qy	781	CTCCACACACACACATCTGGGCGCCCTTAGAGAGCGCAGCATCTGAGCAAAAGAGAGAT	840
Db	1101	CTCCACACACACACATCTGGGCGCCCTTAGAGAGCGCAGCATCTGAGCAAAAGAGAGAT	1160
Qy	841	AAACGAAAGACACCCCTCTC	861
Db	1161	AAACGAAAGACACCCCTCTC	1181

RESULT 8	
AF305616	
LOCUS	4839 bp mRNA linear
DEFINITION	Homo sapiens STAG1/PMEP1 mRNA, complete cds.
ACCESSION	AF305616
VERSION	AF305616.1 GI:16303741

SOURCE ORGANISM	Homo sapiens (human)
	Homo sapiens

REFERENCE 1 (bases 1 to 4839)

AUTHORS	TITLE
Rae, F. K., Hooper, J. D., Nicol, D. L. and Clements, J. A.	Characterization of a novel gene, STAG1/PMEPAL, upregulated in

JOURNAL
PUBMED
REFERENCE
Mol. Carcinog. 32 (1), 44-53 (2001)
11568975
2 (bases 1 to 4839)

AUTHORS Rae, F.K., Hooper, J.D., Nicol, D.L. and Clements, J.A.
TITLE Direct Submission
JOURNAL Submitted (14-SEP-2000) Centre for Molecular Biotechnology,
University of Dundee, Dundee, Scotland, UK

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ORIGIN

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Query Match	100.0%;	Score 861;	DB 8;	Length 4839;
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Oy	61	TCCTGCACGTGCAACTGCAAAAGCTCTTTGTTCCAGACATGAGATACGAGCTGGAG	120
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Oy	121	TTTGTTCAGATCATCATCTGCGTGGTGTATGTATGGTGAATGGATGGATGATCAGTGC	180
Db	441	TTTGTTCAGATCATCATCTGCGTGGTGTATGTATGGTGAATGGATGGATGATCAGTGC	500
Oy	181	CTGCTGAGCCACTACAGCTGTCTGCACGGTCTTTCATCAAGCCGGCAACGCAAGGGCGG	240
Db	501	CTGCTGAGCCACTACAGCTGTCTGCAAGGTCTTTCATCAAGCCGGCAACGCAAGGGCGG	560
Oy	241	AGAGAGAAATATGCTCTGTCTCTCAAGAGATATGCTTGGGCTCTGGAGAGACATGTGCA	300
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Oy	301	GGCAACGGAAATCCCAAGAGCGCAGAGTCTACGCCCGCTCGGCCCAACGACCGCTGACC	360
Db	621	GGCAACGGAAATCCCAAGAGCGCAGAGTCTACGCCCGCTCGGCCCAACGACCGCTGACC	680
Oy	361	GTGCGCGCTTGTGCGCCCAAGCGGAGGCGTTTCCACCGCTTCCAGCCCACTATCCGTACTTG	420
Db	681	GTGCGCGCTTGTGCGCCCAAGCGGAGGCGTTTCCACCGCTTCCAGCCCACTATCCGTACTTG	740
Oy	421	CAGACAGGATTCACCTGCGCAACCCACCATCTCGCTGTCAAGCGGGAGAGAACCCCAACC	480
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Oy	541	GAGTCGATGCGCGGACCCCGCAAAAGAACCATCTTTCACAGTGAACGTGATGATAGTGC	600
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Oy	601	AGGCTGAGCGGAGCCCTGCGCCCGCCAGCAGTAACTCGGAGCATCAGCGCCACGTCGTAACGG	660
Db	921	AGGCTGAGCGGAGCCCTGCGCCCGCCAGCAGTAACTCGGAGCATCAGCGCCACGTCGTAACGG	980
Oy	661	AGCGGCGGAGCCCATGAGAGAGGGGCGCGCGCCCATCAACAGGAGGTCAATGGGCACTAACCG	720
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Oy	721	GGGTCTCTCTTCCAGCACAGCAGAGCAGTGGGCGCGCTCTTGTCTGAGAGGAGCCCGG	780
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Db	1101	CTCCACCAACACATCGCGCGCTCTAGAGCGCAGCATCTGAGCAAAAGAGAGAT	1160
Oy	841	AAACGAAAGGACACCCCTCTC	861
Db	1161	AAACGAAAGGACACCCCTCTC	1181

RESULT 9
LOCUS CS130796 4930 bp DNA linear PAT 02-AUG-2005
DEFINITION Sequence 82 from Patent WO2005064009.
ACCESSION CS130796
VERSION CS130796.1 GI:71792866
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
1 Oerntoft, T.F.
AUTHORS Classification of cancer
TITLE Patent: WO 2005064009-A 82 14-JUL-2005;
JOURNAL Aros Applied Biotechnology APS (DK)
FEATURES
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ORIGIN
Query Match 100.0%; Score 861; DB 6; Length 4930;
Best Local Similarity 100.0%; Pred. No. 1,1e-126;
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 454 TCCTGACGTGCACTGCAAGCGCTCTTTGTTCCAGAGATGAGATCAAGAGCTGAG 513
QY 121 TTTGTTCAATCATCATCATCGTGTGATGATGATGATGATGATGATGATGATGATG 180
DB 514 TTTGTTCAATCATCATCATCGTGTGATGATGATGATGATGATGATGATGATGATG 573
QY 181 CTGCTAGCCACTCAAGCTGTCTGACGCGTCTTATCAAGCCGCAACGAGGGCCG 240
DB 574 CTGCTAGCCACTCAAGCTGTCTGACGCGTCTTATCAAGCCGCAACGAGGGCCG 633
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DB 634 AGAGAGAAAGATCCCTGTCCTGAGAGATGCTGTGCGCTCGGAGAGACAGTGA 693
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QY 361 GTGCGGCGCTTGGCCCAAGCGGAGCGGCTTCAACCGCTTCAAGCCCACTATCC 420
DB 754 GTGCGGCGCTTGGCCCAAGCGGAGCGGCTTCAACCGCTTCAAGCCCACTATCC 813
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QY 481 TACAGAGCGCCCTGCAACCTTCAAGCTTGGGACCCCGAGAGAGAGCTGAACCG 540
DB 874 TACAGAGCGCCCTGCAACCTTCAAGCTTGGGACCCCGAGAGAGAGCTGAACCG 933
QY 541 GAGTCGGTGGCGCAGCCCAACAGAACATCTTGGACAGTGAAGTGAAGTGAAGT 600
DB 934 GAGTCGGTGGCGCAGCCCAACAGAACATCTTGGACAGTGAAGTGAAGTGAAGT 993
QY 601 AGGCTGGGCGGCGCCCGCCCAAGAGATGATCGGGGATCGAGCGCAAGTGTGAG 660
DB 994 AGGCTGGGCGGCGCCCGCCCAAGAGATGATCGGGGATCGAGCGCAAGTGTGAG 1053

QY 661 AGCGCGGGCGCGCATGAGAGGGGCGCGCCCACTTACAGAGATGATGAGGCACTACCG 720
DB 1054 AGCGCGGGCGCGCATGAGAGGGGCGCGCCCACTTACAGAGATGATGAGGCACTACCG 1113
QY 721 GGGTCCTCTTCCAGCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 1114 GGGTCCTCTTCCAGCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1173
QY 781 CTCACCAACACACATGCGCGCCCTTAGAGAGCGGACCATCTTGAAGCAAGAGAGAT 840
DB 1174 CTCACCAACACACATGCGCGCCCTTAGAGAGCGGACCATCTTGAAGCAAGAGAT 1233
QY 841 AAACAGAAAGACACCTCTCTC 861
DB 1234 AAACAGAAAGACACCTCTCTC 1254

RESULT 10
LOCUS AX775889 1383 bp mRNA linear PAT 14-JUL-2003
DEFINITION Sequence 159 from Patent WO03048202.
ACCESSION AX775889
VERSION AX775889.1 GI:32693607
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
1 Matsuda, A. and Muramatsu, S.
AUTHORS NF- κ B activating gene
TITLE Patent: WO 03048202-A 159 12-JUN-2003;
JOURNAL Asahi Kasei Kabushiki Kaisha (JP)
FEATURES
source
1..1383
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
321..1184
/note="unnamed protein product"
/codon_start=1
/protein_id="CAE11644.1"
/db_xref="GI:32693608"
/translation="MHRMGVNSTAAAGQPNVSCCTCKRSLRQSMETLEFVQI
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YGGPTLQIRDEQQLBNRESVRAFPNNRTIRSDLMDSARLGGPCPPSNGGISATC
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KKDKYKQKGPL"

ORIGIN
Query Match 99.8%; Score 859.4; DB 6; Length 1383;
Best Local Similarity 99.9%; Pred. No. 2.4e-126;
Matches 860; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCACCGCTTATGAGGGGTCAACAGACCGCCGCCGCCGCCGCCGCCCAATGTC 60
DB 321 ATGCACCGCTTATGAGGGGTCAACAGACCGCCGCCGCCGCCGCCGCCCAATGTC 380
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DB 381 TCCTGACGTGCACTGCAAGCGCTCTTTGTTCCAGAGATGAGATCAAGAGCTGAG 440
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DB 441 TTTGTTCAATCATCATCATCGTGTGATGATGATGATGATGATGATGATGATGATG 500
QY 181 CTGCTAGCCACTCAAGCTGTCTGACGCGTCTTATCAAGCCGCAACGAGGGCCG 240
DB 501 CTGCTAGCCACTCAAGCTGTCTGACGCGTCTTATCAAGCCGCAACGAGGGCCG 560

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Qy	687	GGCCACCTACAGCGAGGTATCGGCCACTAACCGGGGTCTCTCTTCAGCACCAAGCAGAG	746
Db	727	GGCCACCTACAGCGAGGTATCGGCCACTAACCGGGGTCTCTCTTCAGCACCAAGCAGAG	786
Qy	747	CAGTGGGCGGCTCTTGTGTGAGGGGACCGGCTCCACACACATGCGGCCCT	806
Db	787	CAGTGGGCGGCTCTTGTGTGAGGGGACCGGCTCCACACACATGCGGCCCT	846
Qy	807	AGAGAGCGCAGCATCTGGAGCAAGAGATTAACAGAAAGACACCTCTC	861
Db	847	AGAGAGCGCAGCATCTGGAGCAAGAGATTAACAGAAAGACACCTCTC	901

Search completed: February 28, 2006, 12:48:11
Job time : 4613.99 secs

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OM nucleic - nucleic search, using bw model

Run on: February 28, 2006, 08:23:08 ; Search time 586.364 Seconds
(without alignments)
9786.244 Million cell updates/sec

Title: US-09-934-249-3

Perfect score: 861
Sequence: 1 atgcacccgttgatgagggggt.....aacagaaaggacacctctc 861

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

- N_Geneseq_21:*
- 1: geneseqn1980s:*
 - 2: geneseqn1990s:*
 - 3: geneseqn2000s:*
 - 4: geneseqn2001as:*
 - 5: geneseqn2001bs:*
 - 6: geneseqn2002as:*
 - 7: geneseqn2002bs:*
 - 8: geneseqn2003as:*
 - 9: geneseqn2003bs:*
 - 10: geneseqn2003cs:*
 - 11: geneseqn2003ds:*
 - 12: geneseqn2004as:*
 - 13: geneseqn2004bs:*
 - 14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	861	100.0	864	11	ADN38809 Cancer/an
2	861	100.0	1321	6	ABK12137 Human CDN
3	861	100.0	4519	13	ADX97454 Pancreat
4	861	100.0	4839	8	ACC49552 Tumour-as
5	861	100.0	4839	11	ADP65809 Human STA
6	861	100.0	4839	11	ADP65729 Human tra
7	861	100.0	4839	12	ADM67045 Human hom
8	861	100.0	4839	13	ADR65875 Human pro
9	861	100.0	4839	13	ADR66778 Human pro
10	861	100.0	4839	13	ADU06063 Novel bry
11	861	100.0	4839	14	ADM43368 Prostate
12	861	100.0	4931	13	ACM40804 Tumour-as
13	861	100.0	4930	14	ABE22787 Human col
14	859.4	99.8	1383	10	ADC37326 Nuclea
15	755.2	87.7	969	3	AAA75151 CDNA enco
16	754.2	87.6	1140	6	ABK92120 Prostate
17	754.2	87.6	1141	10	ADP75588 Prostate
18	754.2	87.6	1850	8	ACC49536 Tumour-as
19	754.2	87.6	4527	11	ADL83313 Human and

20	754.2	87.6	4527	14	ADP85880 Human ARP
21	754.2	87.6	4538	14	ABE22832 Human col
22	753.6	87.5	969	3	AAA75164 CDNA clon
23	753.6	87.5	969	3	AAA75163 CDNA clon
24	753.6	87.5	969	3	AAA75165 CDNA clon
25	753.6	87.5	1140	10	AA660105 Human and
26	753.6	87.5	1140	10	ADP62276 Human and
27	753.6	87.5	1140	12	ADP39826 Human PME
28	752.8	87.4	759	10	ADP17545 Human and
29	752.8	87.4	759	10	ADP62277 Human PME
30	752.8	87.4	759	12	ADP39827 Human PME
31	752.6	87.4	806	3	ACC49537 Tumour-as
32	752.6	87.4	1061	3	AAA47429 Sequence
33	752.6	87.4	1085	10	ADP37324 Nuclea
34	752.6	87.4	1334	8	ABE26103 Human sec
35	752.6	87.3	4531	14	ABE22833 Human col
36	742.4	86.2	1066	4	AA159654 Human pol
37	712	82.7	1069	4	AA157868 Human pol
38	612.4	71.1	878	6	ABK12142 Mouse CDN
39	544.4	63.2	1583	6	ABE61424 Human pro
40	462.2	53.7	1713	3	AAA75152 CDNA enco
41	460.6	53.5	1713	3	AAA75167 CDNA clon
42	460.6	53.5	1713	3	AAA75166 CDNA clon
43	460.6	53.5	1713	3	AAA75168 CDNA clon
44	445.6	51.8	693	6	ABK12143 Human MIV
45	417.4	48.5	812	2	AAZ52964 Human pro

ALIGNMENTS

RESULT 1	
ADN38809	ADN38809 standard; cDNA; 864 BP.
ID	
XX	ADN38809;
AC	
DT	17-JUN-2004 (first entry)
DE	Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:127.
XX	
XX	Human; differential expression; cancer; angiogenic disorder;
KW	fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW	inflammatory disease; autoimmune disease;
KW	retinal neovascularisation syndrome; scarring; uterine fibroid;
KW	detection; diagnosis; prognosis; drug screening; drug targeting;
KW	wound healing; contraception; cytostatic; cardiatic; immunomodulatory;
KW	vulnerable; gene therapy; vaccine; gene; ss.
OS	Homo sapiens.
XX	
PN	WO2003042661-A2.
XX	
PD	22-MAY-2003.
XX	
EF	13-NOV-2002; 2002WO-US036810.
XX	
XX	13-NOV-2001; 2001US-0350666P.
PR	21-NOV-2001; 2001US-0332464P.
PR	29-NOV-2001; 2001US-0334393P.
PR	03-DEC-2001; 2001US-0335394P.
PR	14-DEC-2001; 2001US-0340376P.
PR	08-JAN-2002; 2002US-0347211P.
PR	10-JAN-2002; 2002US-0347349P.
PR	08-FEB-2002; 2002US-0355250P.
PR	13-FEB-2002; 2002US-0356714P.
PR	20-FEB-2002; 2002US-0359077P.
PR	29-MAR-2002; 2002US-0368809P.
PR	04-APR-2002; 2002US-0370110P.
PR	12-APR-2002; 2002US-0372246P.
PR	05-JUN-2002; 2002US-0386614P.
PR	16-JUL-2002; 2002US-0396839P.
PR	22-JUL-2002; 2002US-0397775P.


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Db 741 CAGCAGAGATGACCTGCGACCCACCATCTGCTGTGACAGCGGGAGAGCCCCCAACC 800
QY 481 TACCAAGGAGCCCTGCACTCTGAGCTTCGGGACCCCGACAGAGCTGGAATGAAACCGG 540
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QY 541 GAGTGGGTGCGGCGACCCCAACAGAACCATCTTGTGACAGTGAAGCTGATGATGTC 600
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Db 861 GAGTGGGTGCGGCGACCCCAACAGAACCATCTTGTGACAGTGAAGCTGATGATGTC 920
QY 601 AGGCTGGGAGGCGCCCGCCCGCCAGCAGTAATCGGGGATGACGCGCATGCTAGCGC 660
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QY 661 AGCGGCGGCGCATGAGAGGGGCGCGCCGACCTTACAGGAGGTCAATCGGCACTAACCGG 720
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QY 781 CTCCACCAACACACATCGCGCCCTTACAGAGGCGAGCCATCTGAGCAAGAGAGAGAT 840
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Db 1161 AAACAGAAAGACACCTCTCTC 1181
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```
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ID ADP65729 standard; DNA; 4839 BP.
```

```
XX AC ADP65729;
```

```
XX DT 12-AUG-2004 (first entry)
```

```
XX DE Human transmembrane, prostate androgen induced RNA (TMEMPA1), DNA.
```

```
XX KW autoimmune disease; arthritis; gene expression analysis;
```

```
XX KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
```

```
XX KW antiarthritis; osteopathic; antigout; antiinflammatory; dermatological;
```

```
XX KW immunomodulatory; lupus; ankylosing spondylitis; fibrositis;
```

```
XX KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
```

```
XX KW immune; ds; human.
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XX OS Homo sapiens.
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XX PN WO2003072827-A1.
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XX PD 04-SEP-2003.
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XX PF 31-OCT-2002; 2002WO-US035433.
```

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XX PR 31-OCT-2001; 2001US-0336220P.
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XX PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
```

```
XX PI Hirsch R, Thornton SL;
```

```
XX DR WPI; 2003-712740/67.
```

```
XX DR GENBANK; NM_020182.
```

```
XX PT Diagnosing and analyzing autoimmune disease using gene expression
```

```
XX PT profiles and microarray technology, useful for diagnosing and treating
```

```
XX PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
```

```
PS Disclosure; Page; 56P; English.
XX
XX The invention relates to a novel method for diagnosing and analysing
CC autoimmune disease or arthritis. The method comprises obtaining a
CC patient sample containing mRNA, analysing gene expression using the mRNA
CC that results in a gene expression signature of the mRNA, and using that
CC gene expression signature to diagnose or analyse the autoimmune disease
CC or arthritis in the patient, where gene expression of at least 60% of
CC the genes correlates with that of the gene signature. The invention
CC further comprises: a treatment of rheumatoid arthritis; identification
CC of genes for targeting in the treatment of rheumatoid arthritis in a mammal;
CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
CC analysis of autoimmune disease or rheumatoid arthritis; screening the
CC efficacy of a candidate drug in vitro for the treatment of collagen-
CC induced arthritis; and reducing the symptoms associated with collagen-
CC induced arthritis. The compositions of the invention have the following
CC activities: immunosuppressive, antirheumatic, antiarthritis, osteopathic,
CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
CC methods and compositions of the present invention are useful for
CC diagnosing and treating autoimmune disease or arthritis, such as
CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
CC immune disease caused by an infectious agent. This polynucleotide
CC represents a DNA sequence relating to the genes used in the analysis and
CC treatment of autoimmune diseases or arthritis. Note: This sequence is
CC not shown in the specification. It has been supplied in an electronic
CC format from WIPO.
```

```
XX SQ Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;
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XX Query Match 100.0%; Score 861; DB 11; Length 4839;
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XX Best Local Similarity 100.0%; Pred. No. 3,3e-167;
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XX Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

```
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```

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```

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```

```
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```

```
QY 481 TACCAAGGAGCCCTGCACTCTGAGCTTCGGGAGCCCGACAGAGCTGGAATGAAACCGG 540
```

```
Db 801 TACCAAGGAGCCCTGCACTCTGAGCTTCGGGAGCCCGACAGAGCTGGAATGAAACCGG 860
```

```
QY 541 GAGTGGGTGCGGCGACCCCAACAGAACCATCTTGTGACAGTGAAGCTGATGATGTC 600
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RESULT 8
AD65875
ID AD65875 standard; DNA; 4839 BP.
XX
AC AD65875;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human prostatic carcinoma derived DNA SEQ ID 71 #1.
XX
KM human; cytostatic; diagnosis; prostatic cancer;
XX differential expression analysis; ds.
OS Homo sapiens.
XX
PN WO2004076614-A2.
XX
PD 10-SEP-2004.
XX
PF 22-FEB-2004; 2004WO-DE000433.
XX
PR 27-FEB-2003; 2003DE-01009985.
XX 14-MAY-2003; 2003DE-01022134.
XX
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILARSKY C. PILARSKY C.
XX
PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;
PI Schmitt A, Beckmann G, Bruemendorf T, Kinemann H, Roepcke S;
PI Kinzhong L, Staub E;
XX
DR WPI; 2004-653386/63.
XX
PT New nucleic acids, and encoded proteins, from prostatic cancer tissue,
PT useful for diagnosis, treatment and in screening for specific binding
PT agents.
XX
PS Claim 1; Page 277; 1607pp; German.
XX
CC This invention describes novel cytostatic polynucleotide and polypeptide
CC sequences which can be used in a method for diagnosing prostatic cancer
CC or the risk of developing prostatic cancer. Diagnosis is based on
CC determining over transcription or over expression of the sequences in
CC prostatic tissue. Screening for inhibitors of the sequences or detection
CC substances involves a binding assay, any compounds that bind are
CC selected, optionally after deconvolution of mixtures. Detection of a
CC predetermined minimum level of the reporter indicates the presence of
CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
CC short-interfering RNA or ribozymes; an organic molecule of molecular
CC weight below 5000, preferably 300, that binds to the polypeptide; an
CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human
CC (monoclonal) antibody directed against Ab or any of the above derivatised
CC with a reporter group, cell toxin, immunostimulatory molecules and/or
CC radioisotopes. The polynucleotides are identified in human prostatic
CC cancer by differential expression analysis, using DNA microarrays,
CC between normal and tumorous tissues, with (over)expression being detected
CC by quantitative PCR. Analysis of prostatic cancer samples showed that
CC CD24 was upregulated in many of them. Sections of tissue, isolated from
CC prostatic cancer patients, or subjects at risk, were incubated
CC sequentially with anti-human CD4 murine monoclonal antibodies;
CC biotinylated second antibody; streptavidin-conjugated horseradish
CC peroxidase and then diamnobenzydine as colour former (brown). The
CC samples were counterstained with hemalum (blue). Malignant cells stained
CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
CC lymph node metastases were also stained. AD65805-AD65954 represent the
CC polynucleotide and polypeptide sequences used in the method of the

CC invention.
XX
SQ Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;
Query Match 100.0%; Score 861; DB 13; Length 4839;
Best Local Similarity 100.0%; Pred. No. 3.3e-167;
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCACCGCTTGATGGGGGTCAACAGCACCGCCGCGCGCGCGGACCCCAATGTC 60
DB 321 ATGCACCGCTTGATGGGGGTCAACAGCACCGCCGCGCGCGCGGACCCCAATGTC 380
QY 61 TCCTGACGTCGAATGCAAGAGCTCTTGTTCAGACATGAGATCAAGGAGCTGAG 120
DB 381 TCCTGACGTCGAATGCAAGAGCTCTTGTTCAGACATGAGATCAAGGAGCTGAG 440
QY 121 TTTGTTGATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 180
DB 441 TTTGTTGATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 500
QY 181 CTGCTGAGCCACTACAGAGCTGTGTGACGCTTTCATCAGCCGACACAGGAGGCGG 240
DB 501 CTGCTGAGCCACTACAGAGCTGTGTGACGCTTTCATCAGCCGACACAGGAGGCGG 560
QY 241 AGGAGAGAGAGATGCCCTGCTCAGAGAGATGCTGTGAGGCTCGGAGAGCAAGTCA 300
DB 561 AGGAGAGAGAGATGCCCTGCTCAGAGAGATGCTGTGAGGCTCGGAGAGCAAGTCA 620
QY 301 GGCACAGGATCCCAAGAGCCGAGGCTTACGCGCCGCTCGGACCAAGCCGCTGAGC 360
DB 621 GGCACAGGATCCCAAGAGCCGAGGCTTACGCGCCGCTCGGACCAAGCCGCTGAGC 680
QY 361 GTGCGCGCCCTTGCCCAAGGAGGCTTCCACGCGCTTCCAGCCCACTATCCGACTCG 420
DB 681 GTGCGCGCCCTTGCCCAAGGAGGCTTCCACGCGCTTCCAGCCCACTATCCGACTCG 740
QY 421 CAGCAGAGATGACCTGACCCCACTCATCTGCTGAGAGCGGAGAGAGGCCCAACC 480
DB 741 CAGCAGAGATGACCTGACCCCACTCATCTGCTGAGAGCGGAGAGAGGCCCAACC 800
QY 481 TACAGGGGCCCTGACCCCTTCAGGCTTGGGAGCCCGAGCAGACAGCTGGAACCGG 540
DB 801 TACAGGGGCCCTGACCCCTTCAGGCTTGGGAGCCCGAGCAGACAGCTGGAACCGG 860
QY 541 GAGTGGTGGCGGCAACCCCAAGAACCAATCTTCAGACGAGACCTGATGATGTC 600
DB 861 GAGTGGTGGCGGCAACCCCAAGAACCAATCTTCAGACGAGACCTGATGATGTC 920
QY 601 AGGCTGGGGGCGCCGCGCCCGCAGAGTACTGGGATCAGGCGCCACGTGTAACGGC 660
DB 921 AGGCTGGGGGCGCCGCGCCCGCAGAGTACTGGGATCAGGCGCCACGTGTAACGGC 980
QY 661 AGCGGCGGGCGATGAGAGGGGCGCGCCCACTTACAGGAGATCATGGCCACTTACCGG 720
DB 981 AGCGGCGGGCGATGAGAGGGGCGCGCCCACTTACAGGAGATCATGGCCACTTACCGG 1040
QY 721 GGGTCTCTCTTCCAGACCAAGAGCAAGTGGGCGGCTCTTCTTGGAGGGGACCGG 780
DB 1041 GGGTCTCTCTTCCAGACCAAGAGCAAGTGGGCGGCTCTTCTTGGAGGGGACCGG 1100
QY 781 CTCACCAACACACATGCGCGCCCTTACAGAGCGAGGACCATCTGAGCAAGAGAT 840
DB 1101 CTCACCAACACACATGCGCGCCCTTACAGAGCGAGGACCATCTGAGCAAGAGAT 1160
QY 841 AAACAGAAAGACACCTCTC 861
DB 1161 AAACAGAAAGACACCTCTC 1181
RESULT 9
AD66778
ID AD66778 standard; DNA; 4839 BP.
XX

Db	453	TCCTGCACTGTCACACTGCATAACGCTCTTTGTTCCAGAGCACTGAGATCAACGAACTGGAG	512
Qy	121	TTTGTTCAGATCATCATCATCTGTGTGTGTGATGATGTGTGTGTGTGTATCACTGC	180
Db	513	TTTGTTCAGATCATCATCATCTGTGTGTGTGTGATGATGATGATGATGTGTGTATCACTGC	572
Qy	181	CTGCTGAGCCACTACAGCTGTCTGTGCAAGGTCCTTCATCAACCCGGACAAGCCTAAGGGCCG	240
Db	573	CTGCTGAGCCACTACAGCTGTCTGTGCAAGGTCCTTCATCAACCCGGACAAGCCTAAGGGCCG	632
Qy	241	AGGAGAGAAATGACCCTGTCTCTCCAGAAAGATGACCTGTGGCCCTGGAGAGCAGACTGTCA	300
Db	633	AGGAGAGAAATGACCCTGTCTCTCCAGAAAGATGACCTGTGGCCCTGGAGAGCAGACTGTCA	692
Qy	301	GGCAACGAAATCCAGAGCCGCAAGGCTTACGCCCCCGCTCGGACCCACGACCGCTGGCC	360
Db	693	GGCAACGAAATCCAGAGCCGCAAGGCTTACGCCCCCGCTCGGACCCACGACCGCTGGCC	752
Qy	361	GTGCCCGCTTTGCGCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACTTATCCGTACTTG	420
Db	753	GTGCCCGCTTTGCGCCAGCGGGAGCGCTTCCACCGCTTCCAGCCCACTTATCCGTACTTG	812
Qy	421	CAGACACGAGATCGACCTGTGCAACCCACATCTGCGTGTAGAAGGGGAGAGACCCCAACC	480
Db	813	CAGACACGAGATCGACCTGTGCAACCCACATCTGCGTGTAGAAGGGGAGAGACCCCAACC	872
Qy	481	TACACGAGACCCCTGTGCAACCTCCAGCTTTCGGGACCCCGACGACAGCTTGAACTGAACCG	540
Db	873	TACACGAGACCCCTGTGCAACCTCCAGCTTTCGGGACCCCGACGACAGCTTGAACTGAACCG	932
Qy	541	GAGTCGGTGGCGCAACCCCAACGAACCATCTTTCGACAGTACCTGATGATGATGTGCC	600
Db	933	GAGTCGGTGGCGCAACCCCAACGAACCATCTTTCGACAGTACCTGATGATGATGTGCC	992
Qy	601	AGGCTGGGCGGCCCCCTGCCCCCGACAGTAACTGGGATATGAGGCCACGCTGTAACGGC	660
Db	993	AGGCTGGGCGGCCCCCTGCCCCCGACAGTAACTGGGATATGAGGCCACGCTGTAACGGC	1052
Qy	661	AGCGGCGGCGCATGAGAGGGGCGGCGGCCACTTACAGCGAGGTATCGGCCACTTACCGG	720
Db	1053	AGCGGCGGCGCATGAGAGGGGCGGCGGCCACTTACAGCGAGGTATCGGCCACTTACCGG	1112
Qy	721	GGGTCCTCTTTCAGACACCGACGAGCAGTGTGGCCGCCCTCTCTTGTCTGAGAGGGACCCGG	780
Db	1113	GGGTCCTCTTTCAGACACCGACGAGCAGTGTGGCCGCCCTCTCTTGTCTGAGAGGGACCCGG	1172
Qy	781	CTCCACACACACACATGCGGCGCCTTAGAGAGCGCAGCATTGTGAACAAAGAAAGAT	840
Db	1173	CTCCACACACACACATGCGGCGCCTTAGAGAGCGCAGCATTGTGAACAAAGAAAGAT	1232
Qy	841	AAACGAAAGGACACCTCTC	861
Db	1233	AAACGAAAGGACACCTCTC	1253

RESULT 13	
AE8B22787	
ID	AE8B22787 standard; DNA; 4930 BP.
XX	
AC	
XX	AE8B22787;
DT	
XX	22-SEP-2005 (first entry)
DE	
XX	Human colon cancer-associated gene SEQ ID NO:82.
XX	
KW	cancer; genetic marker; lymphoma; cytostatic; hematological disease;
KW	immune disorder; neoplasm; colon tumor; gastrointestinal disease;
KW	adenocarcinoma; carcinoma; screening; diagnostic; prognostic;
KW	pharmaceutical; ds; gene.
XX	
OS	Homo sapiens.
XX	

PN	WO2005064009-A1.
XX	
PD	14-JUL-2005.
XX	
PF	23-DEC-2004; 2004WO-DK000914.
XX	
PR	27-DEC-2003; 2003DK-00001940.
PR	24-JAN-2004; 2004DK-00000096.
PR	07-APR-2004; 2004DK-00000586.
PR	26-NOV-2004; 2004DK-00001843.
XX	
PA	(AROS-) AROS APPLIED BIOTECHNOLOGY APS.
PI	Orntofc TF, Jensen JL, Krnhofer M, Laino P, Aalonen LA;
XX	
XX	WPI; 2005-506661/51.
XX	
PT	Classifying the cancer in an individual having contracted cancer
PT	comprises determining the microsatellite status of the tumor.
XX	
PS	Claim 9, SEQ ID NO 82, 338pp; English.
XX	
CC	The invention relates to a method of classifying the cancer in an
CC	individual having contracted cancer, which comprises determining the
CC	microsatellite status of the tumor. The microsatellite status or the
CC	hereditary or sporadic nature of the cancer is determined by a method
CC	comprising: (a) obtaining a sample from the individual having contracted
CC	cancer, the sample comprising gene expression products, the presence
CC	and/or amount of which forms a pattern that is indicative of the
CC	microsatellite status or the hereditary or sporadic nature of the cancer;
CC	(b) determining the presence and/or amount of the gene expression
CC	products forming the pattern, and obtaining an indication of the
CC	microsatellite status or the hereditary or sporadic nature of the cancer
CC	in the individual based on step (b). At least one or two of the gene
CC	expression products forming a pattern used to determine the
CC	microsatellite status or the hereditary or sporadic nature of the cancer
CC	are selected individually from any of the 134 genes comprising 367-7850
CC	bp (ABE22706 to ABE22833), given in the specification. Also included are:
CC	a method for treating an individual; a method for reducing malignancy of
CC	a cell; a method for producing antibodies against an expression product
CC	of a cell from a biological tissue; pharmaceutical composition, for
CC	treating a classified cancer, comprising at least one antibody, an assay,
CC	one polypeptide, or at least one nucleic acid and/or probe; and an assay,
CC	for classification of cancer in an individual having contracted cancer,
CC	comprising at least one marker capable of determining the microsatellite
CC	status in a sample and at least one marker in a sample determining the
CC	prognostic marker, where the microsatellite status and the prognostic
CC	marker is determined simultaneously or sequentially. The method above is
CC	useful for producing an assay for classifying cancer in animal tissue.
CC	The peptide, gene, or probe is useful for preparing a pharmaceutical
CC	composition for the treatment of a cancer in animal tissue. The method is
CC	useful for classifying the cancer in an individual having contracted
CC	cancer, i.e. colon cancer, e.g. an adenocarcinoma, a carcinoma, a
CC	teratoma, a sarcoma, and/or a lymphoma. The present sequence represents a
CC	colon cancer-associated gene used in the method of the invention.
XX	
SQ	Sequence 4930 BP, 1133 A, 1331 C, 1324 G, 1142 T, 0 U, 0 Other;
XX	
Query Match	100.0%; Score 861; DB 14; Length 4930;
Best Local Similarity	100.0%; Pred. No. 3.3e-167;
Matches 861; Conservative	0; Mismatches 0; Indels 0; Gaps 0
QY	1 ATGCACCGCTTGATGGGGGTCAACAGACCGCGCGCGCGCGGAGCCCAATGTC 60
DB	394 ATGCACCGCTTGATGGGGGTCAACAGACCGCGCGCGCGCGGAGCCCAATGTC 453
QY	61 TCTGTGACGTGCAACTGCAACGCTTTTGTTCACAGATGGAGATCACGAGCTGGAG 120
DB	454 TCTGTGACGTGCAACTGCAACGCTTTTGTTCACAGATGGAGATCACGAGCTGGAG 513
QY	121 TTGTGTTCATCATCATCATCGGGGATGATGATGGTATGGTGTGATCACTGC 180
DB	514 TTGTGTTCATCATCATCATCGGGGATGATGATGGTATGGTGTGATCACTGC 573

QY	181	TTGCTGAGGACCTTCAAGCTGTGTGCAAGGGTCTTTCAATCAACCGGCACAGCCAGGGCCGG	240
Db	574	CTGCTGAGCCCTTACAGAGCTGTCTTGCAAGGTCTTTATCAAGCCGGCACAGCCAGGGCCGG	633
QY	241	AGGAGAGAAAGATGCGCTGTCTTCAGAAAGATGCTGTGGCCCTCGAGAGCACAGTGTCA	300
Db	634	AGGAGAGAAAGATGCGCTGTCTTCAGAAAGATGCGTGTGGCCCTCGAGAGCACAGTGTCA	693
QY	301	GGCAACGGAAATCCAGAGGCGGAGGTCTAAGCCCGCGCTCGGGCCACCCGACCGCTTGCC	360
Db	694	GGCAACGGAAATCCAGAGGCGGAGGTCTAAGCCCGCGCTCGGGCCACCCGACCGCTTGCC	753
QY	361	GTGCGCGCCCTTCGCGCAGGGGAGGGCTTCCACCGCTTCAGAGCCACCTATCCGMACTGG	420
Db	754	GTGCGCGCCCTTCGCGCAGGGGAGGGCTTCCACCGCTTCAGAGCCACCTATCCGMACTGG	813
QY	421	CAGCACAGAGATGACCTGTCCACCCACATCTCGCTGTCAAGCGGGAGAGAGCCGCCACC	480
Db	814	CAGCACAGAGATGACCTGTCCACCCACATCTCGCTGTCAAGCGGGAGAGAGCCGCCACC	873
QY	481	TACCAAGGCCCCCTGTGCACCTTCAGCTTGGGAGCCCGAGCAGCAGCTGAACTGAACCGG	540
Db	874	TACCAAGGCCCCCTGTGCACCTTCAGCTTGGGAGCCCGAGCAGCAGCTGAACTGAACCGG	933
QY	541	GAGTCGTGTGCGCGCACCCCCAAACGAACCATTTGACAGTGAACCTATGATGATGTGCC	600
Db	934	GAGTCGTGTGCGCGCACCCCCAAACGAACCATTTGACAGTGAACCTATGATGATGTGCC	993
QY	601	AGGCTGGGGCGGGCCCCCTGGCCCCCGCAGAGTAACTCGGGCAATCAGCGCCACGCTACGGC	660
Db	994	AGGCTGGGGCGGGCCCCCTGGCCCCCGCAGAGTAACTCGGGCAATCAGCGCCACGCTACGGC	1053
QY	661	AGCGCGGGCGCATGAGGGGGCGCGCGCCACTTACAGCAGGTCAATCGGCCACTTACCGC	720
Db	1054	AGCGCGGGCGCATGAGGGGGCGCGCGCCACTTACAGCAGGTCAATCGGCCACTTACCGC	1113
QY	721	GGGTCCTCTCTTCAGACCAACGAGCAGCAGTGGGGCGCCCTCTCTTGTGAGGGGACCCGG	780
Db	1114	GGGTCTCTCTTCAGACCAACGAGCAGCAGTGGGGCGCCCTCTCTTGTGAGGGGACCCGG	1173
QY	781	CTTCACACACACACATATCGCGCCCTTAAGAGCGGACAGCATCTTGGAGGAAAGAGAGGAT	840
Db	1174	CTTCACACACACACATATCGCGCCCTTAAGAGCGGACAGCATCTTGGAGGAAAGAGAGGAT	1233
QY	841	AAACGAAAGGACACACCTCTTC	861
Db	1234	AAACGAAAGGACACACCTCTTC	1254

RESULT 14
ADC37326
ID ADC37326 standard; DNA; 1383 BP.

AC ADC37326;

DT 18-DEC-2003 (first entry)

DE Nuclear factor kappa B (NF-kappaB) activating gene, SEQ ID 159.

KW Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease
KW cancer; infectious disease; bone disease; AIDS;
KW neurodegenerative disease; ischemic disorder; Antiinflammatory;
KW Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;
KW Neuroprotective; Nootropic; Cardiant; Gene therapy; human; gene; ds
OS Homo sapiens.

PN WO2003048202-A2

PD 12-JUN-2003.

PF 03-DEC-2002; 2002WO-JP012644.

XX 03-DEC-2001; 2001JP-00368692.
PR 05-DEC-2001; 2001US-0335829P.
PR 03-OCT-2002; 2002JP-00291302.
PR 04-OCT-2002; 2002US-0415769P.

PA (ASAH) ASahi KASEI KK.

PI Matsuda A, Muramatsu S;

DR WPI; 2003-505282/47.

XX

PT useful for treating inflammation, autoimmune diseases, cancers, neurodegenerative diseases or

PT ischemic disorders.

PS Claim 4; SEQ ID NO 159; 938bp; English.

CC The present invention relates to novel proteins and their coding
CC sequences (ADBC37166-ADBC37455), which activate nuclear factor kappa B (NF
CC kappaB). The proteins and their coding sequences are useful for treating
CC a disease associated with NF-kappaB activation, such as inflammation,
CC autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
CC neurodegenerative diseases, or ischaemic disorders.

Sequence 1383 BP; 253 A; 505 C; 440 G; 185 T; 0 U; 0 Other;

Query Match	99.8%;	Score 859.4;	DB 10;	Length 1383;
-------------	--------	--------------	--------	--------------

Matches 860; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ATGCACCGCTGATGGGGTCAACAGCACCGCGCGCGCGCGGCGAGCCCAATGTC 60

Db 321 ATGCACCGCTTGATGGGGTCAACAGCACCGCCGCCGCCGCCGCCGAGCCCAATGTC 380

61 TCCTGCACGTGCAACTGCMAACGCTCTTTGTTCCAGAGCATGGAGATCACGGAGCTGGAG 120

Db 381 TCCTGCACGTGCACTGCAACGCTCTTTGTTCCAGAGCATGGAGATCACGGAGCTGGAG 440

121 TTTGTT CAGATCATCATCGTGGTGATGATGGTGGTGATCACCCTGC 180

Db 441 TTTGTTCAGATCATCATCGTGGTGATGATGGTGGTGATCACCCTGC 500

181 CTGCTGAGCCACTACAAGCTGTCTGCA CGGTCTTCATCAGCCGGCAGCCAGGGCGG 240

Db 501 CTGCTGAGCCACTACAAGCTGTCTGCACGGTCTTCATCAGCCGGCAGCCAGGGCGG 560

241 AGGAGAGAGATGCCCTGTCTCTCAGAAGATGCCCTGTGGCCCTCGGAGAGCACAGTGTCA 300

Db 561 AGGAGAGAGATGCCCTGTCTCAGAAGATGCCCTGTGGCCCTCGGAGAGCACAGTGTCA 620

301 GGCAACGAATCCAGAGCCGCAAGTCTACGCCCGCCTCGGCCACCGACCGCTGGCC 360

Db 621 GGCAACGATCCAGAGCCGCAAGTCTACGCCCGCCTCGGCCCAACGACCGCTGGCC 680

361 GTGCCGCCCTTCGCCACGGGAGCGCTTCCACCGCTTCCAGCCCACTATCCGTACTG 420

Db 681 GTGCCGCCCTTCGCCCAGCGGAGCGCTTCACCGCTTCAGCCCACTATCCGTACTG 740

421 CAGCAGGATCGACTGCAACCAATCTGGTGTGAGACGGGAGAGCCCCACCC 480

Db 741 CAGCACCAGATCGACCTGCCGCCACCATCTGCTGTCAGACGGGAGAGCCCCCACC 800

481 TACCAGGGCCCTGCACCTCCAGCTTCGGGACCCGAGCAGCAGCTGGA CTGAACCGG 540

Db 801 TACCAGGGCCCTGCACCTTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAAGTGAACCGG 860

541 GAGTCGGTGGCGCACCCCCAAACAGAACCATCTTCGACAGTGCCTGATGGATAGTGCC 600

Db 861 GAGTCGGTGGCGCACCCCCCAAACAGAACCATCTTCGACAGTGAACCTGATGGATAGTGC 920

QY 601 AGGCTGGGGGCGCCCTGCCCCCAGCAGTAAGTGGGATGAGGCCAGTGTACGGC 660
DB 921 AGGCTGGGGGCGCCCTGCCCCCAGCAGTAAGTGGGATGAGGCCAGTGTACGGC 980
QY 661 AGGCGGCGGCGCATGAGAGGGGCGCGCCCACTACAGGAGGTATCGGCCTACCGG 720
DB 981 AGCGCGCGGCGCATGAGAGGGGCGCGCCCACTACAGGAGGTATCGGCCTACCGG 1040
QY 721 GGGTCTCTCTTCAAGCAGCAGAGCAATGAGGCGCGCTCTCTTGTGAGGGGACCCGG 780
DB 1041 GGGTCTCTCTTCAAGCAGCAGAGCAATGAGGCGCGCTCTCTTGTGAGGGGACCCGG 1100
QY 781 CTCCACCAACACACATGCGCGCCCTAGAGAGGCGAGCAGCATCTGAGCAAGAGAGAT 840
DB 1101 CTCCACCAACACACATGCGCGCCCTAGAGAGGCGAGCAGCATCTGAGCAAGAGAGAT 1160
QY 841 AAACAGAAAGACACCCCTCTC 861
DB 1161 AAACAGAAAGACACCCCTCTC 1181

RESULT 15
ID AAA75151
XX AAA75151 standard; cDNA; 969 BP.

AC AAA75151;

DT 15-JAN-2001 (first entry)

XX cDNA encoding a human TANGO 261 polypeptide.

XX TANGO 266; TANGO 216; TANGO 261; TANGO 262; TANGO 267;
XX cellular proliferation; cellular differentiation; cellular adhesion;
XX von Willebrand factor-associated disorder; cell trafficking; cancer;
XX hemolipietic associated disease; atelectasis; pulmonary congestion;
XX oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
XX intestinal disorder; spleen associated disease; renal disorder;
XX cardiovascular disorder; ischemic heart disease; hydrocephalus;
XX brain herniation; iatrogenic disease; inflammation; meningitis;
XX Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease;
XX multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 6..764
XX FT /*tag= a
XX FT /product= "TANGO 261"
XX FT 6..89
XX FT sig_peptide /*tag= b
XX FT 90..764
XX FT mat_peptide /*tag= c

XX WO20052022-A1.

XX 08-SEP-2000.

XX 01-MAR-2000; 2000WO-US005226.

XX 01-MAR-1999; 99US-012458P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Barnes TM, Holtzman DA, Sharp JD, Fraser CC;

XX WPI; 2000-579269/54.

XX P-PSDB; AAB18449.

XX Novel human and murine secreted proteins designated TANGO 216, 261, 262,
XX 266 and 267 useful as modulating agents of cellular processes, e.g. for
XX treating cancer.

XX Claim 2; Fig 5; 175pp; English.

XX The present sequence encodes a human TANGO 261 polypeptide. The
XX specification also describes TANGO 266, TANGO 216, TANGO 262, and TANGO
XX 267. The TANGO polypeptides can be used to modulate cellular
XX proliferation, modulate cellular differentiation and/or modulate cellular
XX adhesion. The proteins can be used to treat any von Willebrand factor-
XX associated disorder, regulate extracellular matrix structuring, cellular
XX adhesion, and cell trafficking and/or migration, modulate cellular
XX interactions, modulate cell adhesion in proliferative disorders, such as
XX cancer, modulate the proliferation, differentiation, and/or function of
XX cells that appear in the bone marrow, and leukocytes, treat bone marrow,
XX blood and hematopoietic associated diseases and disorders, atelectasis,
XX pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial
XX asthma and bronchiectasis, intestinal disorders, spleen associated
XX diseases, modulate renal disorders, treat cardiovascular disorders such
XX as ischemic heart disease, modulate the proliferation, differentiation,
XX and/or function of bone and cartilage cells and to treat bone and/or
XX cartilage associated diseases or disorder. They may also be used to treat
XX disorders associated with the ovaries, cerebral oedema, hydrocephalus,
XX brain herniations, iatrogenic disease, inflammation, bacterial and viral
XX meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's
XX disease, multiple sclerosis, brain cancers, hydrocephalus and
XX encephalitis, and treat hepatic disorders

Sequence 969 BP; 211 A; 316 C; 294 G; 148 T; 0 U; 0 Other;

Query Match 87.7%; Score 755.2; DB 3; Length 969;
Best Local Similarity 99.6%; Pred. No. 14e-145;
Matches 757; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 102 GGAGATCAAGAGAGCTGAGTTTGTTCAGATCATCATCTGTTGATGATGATGAT 161
DB 2 GGAGATGAGCGAGCTGAGTTTGTTCAGATCATCATCTGTTGATGATGATGAT 61
QY 162 GGTGTGTGATCACTGCTCTGTCAGCACTACAGCTGTCTGACGCTCTTATCAG 221
DB 62 GGTGTGTGATCACTGCTCTGTCAGCACTACAGCTGTCTGACGCTCTTATCAG 121
QY 222 CCGGACAGCGAGGGGCGGAGAGAGATGCGCTGCTGAGAGATGCTGTGCGC 281
DB 122 CCGGACAGCGAGGGGCGGAGAGAGATGCGCTGCTGAGAGATGCTGTGCGC 181
QY 282 CTGGAGAGACAGTGTGAGGAGCAAGAAATCCCAAGCGCAGTCTACGCCCCCTCG 341
DB 182 CTGGAGAGACAGTGTGAGGAGCAAGAAATCCCAAGCGCAGTCTACGCCCCCTCG 241
QY 342 GCCACCGACCGCTGCGCGCTGCGCCCTTGGCCAGCGGAGCGCTTCCAGCTTCCA 401
DB 242 GCCACCGACCGCTGCGCGCTGCGCCCTTGGCCAGCGGAGCGCTTCCAGCTTCCA 301
QY 402 GCCACCTATCTGTTACCTGACAGAGATGAGCTGCACTGACCACTGCTGTGAGA 461
DB 302 GCCACCTATCTGTTACCTGACAGAGATGAGCTGCACTGACCACTGCTGTGAGA 361
QY 462 CGGGAGAGAGCCCACTACAGAGGCGCTGCACTGCACTGCTGAGGAGCCCGAGCA 521
DB 362 CGGGAGAGAGCCCACTACAGAGGCGCTGCACTGCACTGCTGAGGAGCCCGAGCA 421
QY 522 GCACTGGAAGTGAACCGGAGTGGTGTGCGGACCCCAAGCAAGATCTTGTGACAG 581
DB 422 GCACTGGAAGTGAACCGGAGTGGTGTGCGGACCCCAAGCAAGATCTTGTGACAG 481
QY 582 TGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 641
DB 482 TGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 541
QY 642 CAGCGCAAGTCTACAGGAGCGGCGGAGTGAAGGAGGCGCGCCCACTACAGCGCA 701
DB 542 CAGCGCAAGTCTACAGGAGCGGCGGAGTGAAGGAGGCGCGCCCACTACAGCGCA 601
QY 702 GGTGTGTGATCACTGCTCTGTCAGCACTACAGCTGTCTGACGCTCTTATCAG 761
DB 602 GGTGTGTGATCACTGCTCTGTCAGCACTACAGCTGTCTGACGCTCTTATCAG 661

Qy	762	CTTGCTGAGGGGACCCGGCTCCACCA	CACACATCGCGCCCTTAGAGCGCAGCCAT	821
Db	662	CTTGCTGAGGGGACCCGGCTCCACCA	CACACATCGCGCCCTTAGAGCGCAGCCAT	721
Qy	822	CTGAGCAAGAAGAGATTAACAAGAAG	ACACCCCTCTC	861
Db	722	CTGAGCAAGAAGAGATTAACAAGAAG	ACACCCCTCTC	761

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OM nucleic - nucleic search, using sw model

Run on: February 28, 2006, 09:05:04 ; Search time 3986.56 Seconds
(without alignments)
10104.861 Million cell updates/sec

Title: US-09-934-249-3

Perfect score: 861
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Scoring table: IDENTITY NUC
Gapop 10'-0', Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gsa1:*
10: gb_gsa2:*
11: gb_gsa3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	811.8	94.3	1005	AL578575	AL578575 AL578575
C 2	807.6	93.8	1038	AL517150	AL517150 AL517150
3	743.6	86.4	967	BO641849	BO641849 AGENCOURT
4	700	81.3	1046	BM922276	BM922276 AGENCOURT
5	693	80.5	901	CR612083	CR612083 full-length
6	687.8	79.9	945	BU539219	BU539219 AGENCOURT
C 7	686.2	79.7	850	AL558881	AL558881
8	667.4	77.5	916	BO954555	BO954555 AGENCOURT
C 9	667	77.5	867	BX362386	BX362386
10	666.6	77.4	897	AL558882	AL558882
11	662.8	77.0	850	BU602918	BU602918 AGENCOURT
12	648	75.3	780	AY419334	AY419334 Homo sapi
13	637.4	74.0	647	DN992322	DN992322 TC124411
14	607.4	70.5	609	BO636742	BO636742 hdl3h06.Y
15	603.6	70.1	1207	AK008976	AK008976 Mus muscu
16	591.4	68.7	601	DN991959	DN991959 TC113206
17	588.8	67.2	890	CV028567	CV028567 7115 Full
18	578.4	67.2	890	BO690750	BO690750 AGENCOURT
19	570.4	66.2	973	BU169156	BU169156 AGENCOURT
20	568.8	66.0	572	BX641317	BX641317 DKF2686K
C 21	568.2	66.0	782	BO015170	BO015170 UT-H-ED1-
22	550	63.9	551	BM141979	BM141979 if25a11.Y

23	545	63.3	553	8	DN990606	DN990606 TC121025
24	529.8	61.5	894	3	BI851941	BI851941 603379004
C 25	519.4	60.3	729	5	BO575741	BO575741 UT-H-ED1-
C 26	516.8	60.0	730	3	BM677602	BM677602 UT-B-BO1-
C 27	515.2	59.8	728	5	BU683523	BU683523 UT-CF-EC1
28	504	58.5	780	10	AY419335	AY419335 Pan trogl
29	501.6	58.3	588	3	BM483503	BM483503 536869 MA
C 30	496.8	57.7	711	7	CJ028468	CJ028468 CU028468
31	487.8	56.7	1059	1	AL543170	AL543170
32	487.6	56.6	646	10	CG784226	CG784226 FHRC-GT-
33	475.2	55.2	624	10	AY419336	AY419336 Mus muscu
C 34	468	54.4	857	2	BG323347	BG323347 602421733
C 35	465.8	54.1	744	5	BU414421	BU414421 603670223
36	461	53.5	763	3	BI646175	BI646175 603276395
C 37	445.6	51.8	693	1	AT761441	AT761441 W965F07.X
38	445.4	51.7	655	1	BO691705	BO691705 AGENCOURT
39	445.4	51.7	1280	5	BO691500	BO691500 AGENCOURT
40	443.6	51.5	651	6	CB554226	CB554226 MMSF0052
41	440	51.1	899	5	BU196912	BU196912 AGENCOURT
42	432.8	50.3	964	5	BU859860	BU859860 AGENCOURT
43	430	49.9	841	2	BI156703	BI156703 602922119
44	429.6	49.9	646	5	BU859841	BU859841 AGENCOURT
45	428.8	49.8	974	2	BB624904	BB624904

ALIGNMENTS

RESULT 1
LOCUS AL578575/c 1005 bp mRNA linear EST 07-APR-2004
DEFINITION AL578575 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
CDNA clone CS0DX001YC24 3-PRIME, mRNA sequence.
ACCESSION AL578575
VERSION AL578575.3 GI:46257448
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 1005)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:31316780.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Creteilux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
9945.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna/s=CS0DX001B12NP1&c=9945.r.
Location/Qualifiers
1..1005
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DX001YC24"
/cell_type="HELA"
/cell_line="HELA"
/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES

source

ORIGIN

QY	496	ACCCTCCAGCTTCGGGACCCCGAGCAGAGCTGGAATGAACTGGGAGTCCGTCGCGCA	555
Db	530	ACCCTCCAGCTTCGGGACCCCGAGCAGAGCTGGAATGAACTGGGAGTCCGTCGCGCA	471
QY	556	CCCCCAACAGAACCATCTTCGACAGTGA	615
Db	470	CCCCCAACAGAACCATCTTCGACAGTGA	411
QY	616	TGCCCCCCGACGATGTA	675
Db	410	TGCCCCCCGACGATGTA	351
QY	676	GAGGGGGCGCGCCACCTACGACGAGGTCATCCGCACTACCGGGGTCCTCTTCCAG	735
Db	350	GAGGGGGCGCGCCACCTACGACGAGGTCATCCGCACTACCGGGGTCCTCTTCCAG	291
QY	736	CACCAAGCAGAGTGGGCGCGCTCTCTTGCTGAGGGGACCCGGCTCCACCA	795
Db	290	CACCAAGCAGAGTGGGCGCGCTCTCTTGCTGAGGGGACCCGGCTCCACCA	231
QY	796	ATCCGCGCCCTTGAAGAGCGCAGCCATCTGAGCAAAAGAAAGATTTAA	855
Db	230	ATCCGCGCCCTTGAAGAGCGCAGCCATCTGAGCAAAAGAAAGATTTAA	171
QY	856	CCTCTC	861
Db	170	CCTCTC	165

RESULT 3						
BO641849	BO641849	967 bp	mRNA	linear	EST 15-JUL-2007	
LOCUS	AGSCOURT_8287174	NIH_MGC_43	Homo sapiens	cdna clone	IMAGE:6292265	
DEFINITION	5', mRNA sequence.					

ACCESSION	B0641849	GI:21766021
VERSION	B0641849.1	
KEYWORDS	Homo sapiens (human)	
SOURCE	EST.	
ORGANISM	Homo sapiens	

REFERENCE	1 (bases 1 to 967)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC).
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strusberg, Ph.D.

CNA Library Preparation: Rubin Laboratory
CNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: WCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: L1C6M2493 row: 9 column: 18
High quality sequence stop: 571.

FEATURES	Location/Qualifiers
source	1. .967

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1. .967
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   /db_xref="taxon:9606"
   /clone="IMAGE:6292265"
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   /lab_host="DH10B (phage-resistant)"
   /clone_id="NH_MGC_43"
   /note="Organ: eye; Vector: pOT67; Site_1: XhoI; Site_2:
   EcoRI; cDNA made by oligo-dT priming. Directionally
   cloned into EcoRI/XhoI sites using the following 5'
   adaptor: GGCGACGAG(G). Library constructed by Ling Hong
   in the laboratory of Gerald M. Rubin (University of
   California, Berkeley) using Zap-CDNA synthesis kit
   (Stratagene) and Superscript II RT (Life Technologies)."

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Note: this is a NIH_MGC Library.

Query Match	86.4%	Score 743.6;	DB 5;	Length 967;
Best Local Similarity	99.5%	Pred. No. 1.7e-154;		
Matches 746; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0

[illegible]

RESULT 4	BM9222276	1046 bp	mRNA	linear	EST 12-MAR-2002
LOCUS	BM9222276				
DEFINITION	AGENCOURT_6707077 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5754437				
ACCESSION	BM922276				
VERSION	BM922276.1	GI:19372655			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.				

Db 785 CTAAGAGCGGACCCATCTGAGCAAGAGAAAGATTA 824

RESULT 7
AL558881/c 850 bp mRNA linear EST 02-APR-2004
LOCUS AL558881 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
DEFINITION Homo sapiens cDNA clone CS0DU015YF12 3-PRIME, mRNA sequence.
ACCESSION AL558881 GI:46184268
VERSION AL558881.3
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
REFERENCE 1 (bases 1 to 850)
AUTHORS Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:31283014.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by life technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
945.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?ts=CS0DU015DC06NP1c=945.r.
FEATURES
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/clone="CS0DU015YF12"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
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10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 79.7%; Score 686.2; DB 1; Length 850;
Best Local Similarity 99.3%; Pred. No. 9,3e-142; Indels 0; Gaps 0;
Matches 688; Conservative 1; Mismatches 4;

Db 169 GTGATCACGTGCTGCTGAGCCATCAAGCTGTGTGACAGGTCCTTATCATGACCGGAC 228
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Db 850 GTGATCACGTGCTGCTGAGCCATCAAGCTGTGTGACAGGTCCTTATCATGACCGGAC 791
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|
Qy 229 AGCCAGGGGCGAGAGAGAAAGATCCCTGTCTTCAAGAGATGCTGTGGCCTCGAG 288
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Db 790 AGCCAGGGGCGAGAGAGAAAGATCCCTGTCTTCAAGAGATGCTGTGGCCTCGAG 731
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Qy 289 AGCAGAGTGAAGAGAAAGAAATCCAGAGCGGAGTCTACGCCCGCCTCGGCCAC 348
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Db 730 AGCAGAGTGAAGAGAAAGAAATCCAGAGCGGAGTCTACGCCCGCCTCGGCCAC 671
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Qy 349 GACGCGCTGCGCGTCCGCGCTTCCGCGAGCGGAGCGCTTCCACCGCTTCAGGCCAC 408
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Db 670 GACGCGCTGCGCGTCCGCGCTTCCGCGAGCGGAGCGCTTCCACCGCTTCAGGCCAC 611
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Qy 409 TATCCGTACCTGACAGAGATGCACTGCCACCCACCACTTGTGCTGTGACGCGGAG 468
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Db 610 TATCCGTACCTGACAGAGATGCACTGCCCGCCACCTTGTGCTTGTGACGCGGAG 551
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Qy 469 GAGCCCCACCTTACAGAGGCGCCCTGACACCTTCAGCTTGGGAGACCCCGAGCAGACTG 528
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Db 550 GAGCCCCACCTTACAGAGGCGCCCTGACACCTTCAGCTTGGGAGACCCCGAGCAGACTG 491
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Qy 529 GAATCTGAACCGGAGTGTGCGCGGACCCCAAGAAACATCTTTCAGACGTGACTG 588
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Db 490 GAATCTGAACCGGAGTGTGCGCGGACCCCAAGAAACATCTTTCAGACGTGACTG 431
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Qy 709 GGCCTTACCCGGGGTCTCTCTTTCAGACACAGCAGAGAGTGGGCGGCTTGTCTG 768
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Db 310 GGCCTTACCCGGGGTCTCTCTTTCAGACACAGCAGAGAGTGGGCGGCTTGTCTG 251
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Qy 769 GAGGGAACCCGGCTTCACACACACATGCGCGCCCTAGAGAGCGAGCATCTGAGC 828
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Db 250 GAGGGAACCCGGCTTCACACACACATGCGCGCGCCCTAGAGAGCGAGCATCTGAGC 191
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Qy 829 AAAGAGAAGATTAACAAAAGACACCTCTC 861
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Db 190 AAAGAGAAGATTAACAAAAGACACCTCTC 158
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RESULT 8
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LOCUS B0954555
DEFINITION AGNCOURT_8825282 Lupsk1_sciatic_nerve Homo sapiens cDNA clone
IMAGE:6204609 5', mRNA sequence.
ACCESSION B0954555
VERSION B0954555.1 GI:22370033
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
REFERENCE 1 (bases 1 to 916)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
http://image.llnl.gov
Plate: LMNL3626 row: c column: 10
High quality sequence stop: 669.
FEATURES
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/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-GACATCAAGCGGTCCG-3' and
5'-GACTAATTCTGATCGGAGGCGGCCCTT(15)-3'. Size selected >

Oy		630	TAACTCGGGGCAATAGAGCCAGTGTCTTAGGCAGACGGCGGGGCGCATAGAGGGGCCGCGC	683
Dd		388	TAACTCGGGCAATAGAGCCAGTGTCTTAGGCAGACGGCGGGGCGCATAGAGGGGCCGCGC	329
Oy		690	CACCTACAGCAGAGTCATCGGCACATTACCCGGGGTCTCTTCCAGCACCAAGAGAGAG	749
Dd		328	CACCTACAGCAGAGTCATCGGCACATTACCCGGGGTCTCTTCCAGCACCAAGAGAGAG	269
Oy		750	TGGGCGGCTCTTGCTGAGAGGAGACCCTGCTCAACAACAACATCGGCCCCCTAGA	809
Dd		268	TGGGCGGCTCTTGCTGAGAGGAGACCCTGCTCAACAACAACATCGGCCCCCTAGA	209
Oy		810	GAGCGCAGCCATCTGAGCAAAGAGATTAACAGAAAGGACACCCCTTC	861
Dd		208	GAGCGCAGCCATCTGAGCAAAGAGATTAACAGAAAGGACACCCCTTC	157
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RESULT 10				
LOCUS	AL558882	897 bp	mRNA	linear EST 02-APR-2004
DEFINITION	AL558882 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED			
ACCESSION	Homo sapiens cDNA clone CSDDJ015YF12 5-PRIME, mRNA sequence.			
VERSION	AL558882			
KEYWORDS	AL558882.3 GI:46184269			
SOURCE	EST.			
ORGANISM	Homo sapiens (human)			
AUTHORS	Homo sapiens			
TITLE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
JOURNAL	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
COMMENT	Hominidae; Homo. 1 (bases 1 to 897) Li,W.B., Gruber,C., Jeesee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001) On Feb 15, 2001 this sequence version replaced gi:31283015. Contact: Genoscope Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seque@genoscope.cns.fr Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo (dt) primer. Five primers end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 9945.r For more information about this cluster, see http://www.genoscope.cns.fr/cdna?e=CSDDJ015D06QPl&c=9945.r .			
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	/cell_line="JURKAT"			
	/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"			
	/note="1st strand cDNA was primed with a NotI-oligo (dt) primer. Five primers end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."			
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Query Match	77.4%; Score 666.6; DB 1; Length 897;			
Best Local Similarity	99.3%; Pred. No. 2,1e-137;			
Matches	688; Conservative	2; Mismatches	1; Indels	2; Gaps
Oy	169	GTGATCAGTGTGCTGTGAGCCACTATCAAGCTGTCTGCACGGTCTCTTATCATAGCCGGCAC	228	
Dd	1	GTGATCAGTGTGCTGTGAGCCACTATCAAGCTGTCTGCACGGTCTCTTATCATAGCCGGCAC	60	
Oy	229	AGCCAGGGGCGGAGAGGAAGATGCCCTGTCTCTAGAAAGATGCTGAGGCGCTCGAG	288	
Dd	*			

Db	Accession	Source	Organism	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT								
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QY	289	AGCAAGATGTGACGGCAACGGAAATCCCAAGAGCCGACAGGTCTACGGCCCGGCTCTGGCCCAAC	348																		
Db	121	AGCAAGATGTGACGGCAACGGAAATCCCAAGAGCCGACAGGTCTACGGCCCGGCTCTGGCCCAAC	179																		
QY	349	GACCGGCTGGGCGGAGGCGGCGGCTTGGCCAGGAGGAGGGCTTCGACCGCTTCAGCCCAAC	408																		
Db	180	GACCGGCTGGGCGGAGGCGGCGGCTTGGCCAGGAGGAGGGCTTCGACCGCTTCAGCCCAAC	239																		
QY	409	TATCCGTACCTGCAGACAGAGATGACCTGTGCCACCCACATCTGTGCTGTGACAGGGAG	468																		
Db	240	TATCCGTACCTGCAGACAGAGATGACCTGTGCCACCCACATCTGTGCTGTGACAGGGAG	299																		
QY	469	GAGCCCCCACTTACACAGGGGCTCCTTGACCTTCAAGCTTGGGAGCCCGAGACAGACTG	528																		
Db	300	GAGCCCCCACTTACACAGGGGCTCCTTGACCTTCAAGCTTGGGAGCCCGAGACAGACTG	359																		
QY	529	GACCTGAACCGGGAGGTGGTGGGCGGACCCGCCAAACGAACATCTTGAAGTGAAGCTG	588																		
Db	360	GACCTGAACCGGGAGGTGGTGGGCGGACCCGCCAAACGAACATCTTGAAGTGAAGCTG	419																		
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QY	769	GAGGGGAGCCCGGCTTCACACACACACATCGCGCCCTTGAAGAGCGACCATCTGGAGC	828																		
Db	600	GAGGGGAGCCCGGCTTCACACACACACATCGCGCCCTTGAAGAGCGAG-SCATCTGGAGC	658																		
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Db	659	AAAGAGAAAGATTAACAGAAAGACACCTCTTC	691																		
RESULT 11																					
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DEFINITION	AGENCOURT_10016502 NIH MGC 142 Homo sapiens cDNA clone																				
ACCESSION	IMAGE:6497853 5', mRNA sequence.																				
VERSION	BU602918																				
KEYWORDS	BU602918.1 GI:23254677																				
SOURCE	EST.																				
ORGANISM	Homo sapiens (human)																				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.																				
AUTHORS	1 (bases 1 to 850)																				
TITLE	NIH-MGC http://mgc.nci.nih.gov/.																				

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Oy		530	AACCTGAACCGGGAGAGTCGTGGCGGCAGCCCAACAAGAACAATTCTTGAAGTAGACTGA	589
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Oy		590	TGGAATAGTGCAGAGCTGGGCGGCCCCCTGCCAGAGTAATCTCGGGCAATCAGCGCCA	649
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Db		566	CGTGTCTAATCGCAGCGCGGGCGCATATGAGAGGGCGCGCCGACCTTACAGCGATCATCG	625
Oy		710	GCACTTACCCCGGGGTTCTCTTCCAGACCCAGCAGAGAGTAGGGCGCGCTCTCTTGGTGG	769
Db		626	GCACTTACCCCGGGGTTCTCTTCCAGACCCAGCAGAGAGTAGGGCGCGCTCTCTTGGTGG	685
Oy		770	AGGGGACCCGGCTCCACCAACACACATCGCGCCCCCTTAAAGAGCGCACCATCTTGAGCA	829
Db		686	AGGGGACCCGGCTCCACCAACACACATCGCGCCCCCTTAAAGAGCGCACCATCTTGAGCA	745
Oy		830	AAGAGAGGATTAACAGAAAGGACACCTTTC	861
Db		746	AAGAGAGGATTAACAGAAAGGACACCTTTC	777
RESULT 13				
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DEFINITION		DN992322	647 bp mRNA linear EST 17-MAY-2005	
VERSION		DN992322	TC124411 Human adult whole brain, large insert, PCMV expression library Homo sapiens cDNA clone TC124411 5' similar to Homo sapiens transmembrane, prostate androgen induced RNA (TMEMPR1), transcript variant 4, mRNA sequence.	
KEYWORDS		DN992322	EST.	
SOURCE		DN992322.1	GI:66252153	
ORGANISM		Homo sapiens (human)		
REFERENCE		Homo sapiens		
AUTHORS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.		
JOURNAL COMMENT		1 (bases 1 to 647) Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L., Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M., Zhang,X., Jay,G. and He,W. High-throughput cloning of full-length human cDNAs directly from cDNA libraries optimized for large and rare transcripts Unpublished (2005) Contact: Kovacs, KP High Throughput cDNA Cloning Origene Technologies, Inc. (www.origene.com) 6 Taft Court, Suite 100, Rockville, MD 20850, USA Tel: 301 340 3188 Fax: 301 340 8606 Email: cDNA@origene.com This EST submission is part of an on-going human full-length cloning project at Origene Technologies, Inc. Please contact Origene for access. Origene Technologies, Inc. 6 Taft Ct. Suite 100 Rockville, MD 20850 Tel: (301) 340-3188 http://www.origene.com Seq primer: PCMV6 5prime forward vector primer, Origene Technologies Inc. Location/Qualifiers 1..647 /organism="Homo sapiens"		
FEATURES				
SOURCE				

	ORIGIN	Query Match Best Local Similarity 74.0%; Score 637.4; DB 8; Length 647; Matches 638; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY	68 CGTCAACTGCAAAAGCTCTTTGTTCCAGAGCATGAGATCAACGAGCTGGAGTTTCTC 127	
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OY	128 AGATCATCATCATGTGGTGTGATGATGTGATGTGTGTGTGATCACTGCTGCTGA 187	
DB	129 AGATCATCATCATGTGGTGTGATGATGTGATGTGTGTGTGATCACTGCTGCTGA 188	
OY	188 GCCACTCAAGAGCTGTCTGACAGGTCTTCATCAACGCCGACACGCCAGGGCGGAGAGAG 247	
DB	189 GCCACTCAAGAGCTGTCTGACAGGTCTTCATCAACGCCGACACGCCAGGGCGGAGAGAG 248	
OY	248 AAGATGCCCTGTCTCAAGAAGATGAGCTGTGGCCCTCGAGAGACAGCATGTCCAGACAA 307	
DB	249 AAGATGCCCTGTCTCAAGAAGATGAGCTGTGGCCCTCGAGAGACAGCATGTCCAGACAA 308	
OY	308 GAATCCCAAGAGCGCAGAGTCTACGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCTGCGC 367	
DB	309 GAATCCCAAGAGCGCAGAGTCTACGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCTGCGC 368	
OY	368 CATTGCGCCAGCGGAGAGGCTTCCAACGCTTCCAGCCCACTTATCCGTACTTCGACAGAC 427	
DB	369 CATTGCGCCAGCGGAGAGGCTTCCAACGCTTCCAGCCCACTTATCCGTACTTCGACAGAC 428	
OY	428 AGATCGAAGCTGCAACCACTCTCGCTGTGACAGCGGGAGAGAACCCCCCACTTACCAGAG 487	
DB	429 AGATCGAAGCTGCAACCACTCTCGCTGTGACAGCGGGAGAGAACCCCCCACTTACCAGAG 488	
OY	488 GCCCCTGACCCCTCAGCTTCGGGAGACCCCGAGCAGACAGCTGGAACCTGAACCGGAGAGTCGG 547	
DB	489 GCCCCTGACCCCTCAGCTTCGGGAGACCCCGAGCAGACAGCTGGAACCTGAACCGGAGAGTCGG 548	
OY	548 TGGCGGACACCCCAAAGAACCATTTTCGACAGTAGTACCTGATGATATGTGCCAGGCTGG 607	
DB	549 TGGCGGACACCCCAAAGAACCATTTTCGACAGTAGTACCTGATGATATGTGCCAGGCTGG 608	
OY	608 GGCGGCCCTGGCCCCCAGCAGTAATCGGCGCATCAGCG 646	
DB	609 GGCGGCCCTGGCCCCCAGCAGTAATCGGCGCATCAGCG 647	

RESULT 14

B0636742 LOCUS B0636742 DEFINITION hdl3h06.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he ACCESSION B0636742 VERSION B0636742.1 GI:21761201 KEYWORDS EST. Homo sapiens (human)

609 bp mrna linear EST 15-JUL-2002

hdl3h06.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he

Homo sapiens cDNA clone hdl3h06 5', mRNA sequence.

B0636742.1 GI:21761201

EST.

Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 609)
AUTHORS Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A.,
Touchman,D.W., Bouffard,G., Smith,D. and Peterson,K.
Expressed sequence tag analysis of human retina for the NEIbank
Project: Retbindin, an abundant, novel retinal cDNA and alternative
splicing of other retina-preferred gene transcripts
Mol. Vis. 8 (4), 196-204 (2002)
JOURNAL 12107411
PUBMED
COMMENT Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 13 row: h column: 06
Seq primer: M13RPI reverse primer (ABI).
Location/Qualifiers
1..609
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="hd13h06"
/tissue_type="Retina"
/dev_stage="Adult"
/lab_host="EMD110B"
/clone_lib="Human Retina cDNA (Un-normalized,
unamplified): hd/he"
/note="Organ: Eye; Vector: pSPORT1; Neural retina tissue
was dissected from two 80 year old donors with no observed
eye disease. 100ug of total RNA was used for library
construction. A directionally cloned cDNA library in the
pSPORT1 vector (Life Technologies) was constructed at
Bioserve Biotechnology (Laurel MD) essentially following
the protocols of the Superscript Plasmid System full
details of which are contained in the manufacturer's
instruction manual (http://www.lifetech.com/). First
strand synthesis was carried out using a Not I
primer-adaptor
5'-pGACTAGTTCTAGATCGGAGCGGCCCTT(15-3')-3'. EST analysis
was performed on the unamplified library at the NIH
Intramural Sequencing Center (NISC)."

Query Match 70.5%; Score 607.4; DB 5; Length 609;
Best Local Similarity 99.8%; Pred. No. 2.9e-124;
Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

ORIGIN
219 CAGCGGCGACAGCGGCGGAGAGAGATGCGCTGCTCAGAGGATGCGCTG 278
Db 1 CAGCGGCGACAGCGGCGGAGAGAGATGCGCTGCTCAGAGGATGCGCTG 60
279 GCGCTCGAGAGACAGTGTCAAGCAAGGATCCAGAGCGCGAGTCTACCGCCGC 338
Db 61 GCGCTCGAGAGACAGTGTCAAGCAAGGATCCAGAGCGCGAGTCTACCGCCGC 120
339 TCGGCCACCGACCGCTGCGCGCTTTCGCGCCAGCGGAGAGCGCTTCAACGGCTT 398
Db 121 TCGGCCACCGACCGCTGCGCGCTTTCGCGCCAGCGGAGAGCGCTTCAACGGCTT 180
399 CAGGCCCACTATTCGTAAGTGAAGACAGATGCACTGCGCCACCACTTCGCTGTC 458
Db 181 CAGGCCCACTATTCGTAAGTGAAGACAGATGCACTGCGCCACCACTTCGCTGTC 240
459 AGACGGGAGAGAGCGCCCACTTACAGAGGCGCCCTGACCTTCAGCTTGGGAGCCCGGA 518
Db 241 AGACGGGAGAGAGCGCCCACTTACAGAGGCGCCCTGACCTTCAGCTTGGGAGCCCGGA 300
519 GCAGCAGCTGGAACCTGAACCGGAGTGTGTGCGCGACCCCCCAAGAACATCTTTGCA 578

Db 301 GCAGCAGCTGGAATGGAACCGGAGTGTGTGCGCGACCCCCCAAGAACATCTTTGCA 360
Qy 579 CAGTGACCTGATGATGATGTCGACAGCGTGGCGGCCCTTCCGCCCCCACTTAATCTGGG 638
Db 361 CAGTGACCTGATGATGATGTCGACAGCGTGGCGGCCCTTCCGCCCCCACTTAATCTGGG 420
Qy 639 CATAGCGCCACAGTGTACGCGCAGCGGCGGCGATGAGAGGCGCGCGCCCACTTACAG 698
Db 421 CATAGCGCCACAGTGTACGCGCAGCGGCGGCGATGAGAGGCGCGCGCCCACTTACAG 480
Qy 699 CGAGGTCATCGGCGCACTACCCGCGGCTCTCTTCAGACCAAGACAGAGAGTGGCGGCC 758
Db 481 CGAGGTCATCGGCGCACTACCCGCGGCTCTCTTCAGACCAAGACAGAGAGTGGCGGCC 540
Qy 759 CTCTTGCTGAGAGGAGACCGCGCTTCACACACACATCGCGCCCTTACAGAGCGGAGC 818
Db 541 CTCTTGCTGAGAGGAGACCGCGCTTCACACACACATCGCGCCCTTACAGAGCGGAGC 600
Qy 819 CATCTGGAG 827
Db 601 CATCTGGAG 609

RESULT 15
AK008976
LOCUS
DEFINITION Mus musculus adult male stomach cDNA, RIKEN full-length enriched
library, clone:2210418102 product:Nedd4 WW binding protein 4, full
insert sequence.
ACCESSION AK008976.1 GI:12843488
VERSION AK008976
KEYWORDS HTc; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
JOURNAL High-efficiency full-length cDNA cloning
PUBMED Meth. Enzymol. 303, 19-44 (1999)
10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
JOURNAL Normalization and subtraction of cap-trapper-selected cDNAs to
PUBMED prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
11042159
TITLE THE RIKEN Genome Exploration Research Group Phase II Team and the
PUBMED FANTOM Consortium.
AUTHORS Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
5
TITLE The FANTOM Consortium and the RIKEN Genome Exploration Research
REFERENCE Group Phase I & II Team.
AUTHORS Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,952A
FILING DATE: 19-Apr-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,278
FILING DATE: 28-Oct-1996
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 015280-297100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 921 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1...921
OTHER INFORMATION: Clone 22 coding region
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-091-952A-7

Query Match 40.9%; Score 352.2; DB 3; Length 921;
Best Local Similarity 73.1%; Pred. No. 6.2e-69;
Matches 482; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

94 CAGAGCATGAGATCAAGAGCTGAGATTGTTTCAGATCATCATCATCGTGTGATG 153
166 CCGGGCATCTTCACTGAGCTGAGATTGCCCAATCATCATCATCGTGTGATG 225
154 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 213
226 ACGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 285
214 TTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 273
286 TTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 345
274 CTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 333
346 CTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 399
334 CCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 393
400 GCCCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 459
394 CGCTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 453
460 CGCTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 519
454 CTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 513
520 CTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 579
514 CCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 573
580 CCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 639
574 TTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 630

Db 640 TTGAAGATGATTAATAGATGATGATGATGATGATGATGATGATGATGATGATG 699
Qy 631 AACTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 690
Db 700 AACTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 759
Qy 691 AACTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 749
Db 760 AACTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 818

RESULT 4
US-09-091-952A-6
Sequence 6, Application US/09091952A
Patent No. 645832

GENERAL INFORMATION:
APPLICANT: DeCera-Wadleigh, Sevilla D.
Gershon, Elliot S.
Badner, Judith A.
Goldin, Lynn R.
Berrettini, Wade H.
Yoshikawa, Takeo
Sanders, Alan R.
Esterling, Lisa E.

TITLE OF INVENTION: Chromosomal Markers and Diagnostic Tests for Manic-Depressive Illness
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,952A
FILING DATE: 19-Apr-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,278
FILING DATE: 28-Oct-1996
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 015280-297100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8065 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

FEATURE:
NAME/KEY: -
LOCATION: 1...8065
OTHER INFORMATION: Clone 22

FEATURE:
NAME/KEY: CDS
LOCATION: 116...1036
OTHER INFORMATION: Clone 22 coding region
FEATURE:
NAME/KEY: misc_feature

ADDRESSER: Towns and Towns and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94111-3834

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSO for Windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/091.952A
 FILING DATE: 19-Apr-1999
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/029,278
 FILING DATE: 28-Oct-1996
 APPLICATION NUMBER: PCT/US97/19381
 FILING DATE: 28-Oct-1997

ATTORNEY/AGENT INFORMATION:
 NAME: Smith, Timothy L.
 REGISTRATION NUMBER: 35,367
 REFERENCE/DOCKET NUMBER: 015280-297100US

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 867 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..867
 OTHER INFORMATION: Clone 22 isoform 2 alternatively
 spliced coding region

SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 US-09-091-952A-8

Query Match 33.0%; Score 284.2; DB 3; Length 867;
 Best Local Similarity 68.7%; Pred. No. 7.5e-54;
 Matches 45; Conservative 0; Mismatches 143; Indels 63; Gaps 2;

94 CAGAGCATGAGATCACGAGCTGAGTTGTTCAATCATCATCTGCTGCTGATG 153
 |||||
 166 CCGGGCATCTTCAACTCGAGCTGAGTTGCCCAATCATCATCTGCTGCTGATG 225
 |||||
 154 ATGTGATGTGTGTGTGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 213
 |||||
 226 ACGGTATGTGTGTGTGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 285
 |||||
 214 TTGATCAGCCGCGCAGCAGCGGCGGAGGAGAGAGAGATGCCCTGTCTCAGAGATGC 273
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 286 TTGATCAGCCGCGCAGCAGCGGCGGAGGAGAGATGCCCTGTCTCAGAGATGC 329
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 274 CTGTGCGCTTGGAGAGACAGTGTCAAGGACAGGAATCCAGAGCCGCGAGTTACGCC 333
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 330 -----GCCGAGATCATGATCAT 345
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 334 CCGCTGCGGCGCAGCAGCGGCTGCGCGCTTCCGCGCGGAGAGCGGCTTCAC 393
 |||||
 346 GCGCGGCGGCTCAGGAGAGAGTTTACAGCGCGCTTCTTATCCAGAGGAGTGGTTACGC 405
 |||||
 394 CGCTTCCAGCCCACTTCCGTAATCTGACAGCAGAGATGACCTGCGCAGCCAGCATCTCG 453
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 406 CGCTTCCAGCCCACTTCCGTAATCTGACAGCAGAGATGATCTTCTCCACCATCTCC 465
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 454 CTGTCAAGCGGAGAGAGCGCCCACTTCCAGAGGCGCTTCCAGCTTCCAGCTTCCGAGAC 513
 |||||

DB 466 CTGTCCAGCGGTGAAGAGACACTCTTACAGAGGAGCCCTTGACCTTCGAGCTCCGGGAGC 525
 |||||
 QY 514 CCGAGCAGCAGCTGGAAGTGAACCGGAGAGTGTGCGCGACCCCAAGAGAACATC 573
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 DB 526 CCTGAACAGCAGATGGAATCAACCGAGAGTCCGAGAGGCCCAACCAACAGATCA 585
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 QY 574 TTGACAGTGAAGCTGATGGAATGATGACAGG---CTGGGCGGCGCTGCGCCCGAGCACT 630
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 DB 586 TTGACAGTGAATTTATATAGACATTTCTATGTATAGCGGGGATTCATGCCACCGACAGC 645
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 QY 631 AACTCGGCGATGAGCGCCAGCTGCTTACAGCGAGCGGCGGCGGATGAGAGGCGCGCGCC 690
 |||||
 DB 646 AACTCGGCGATGAGCGAGCAGCAGCTGCGAGCACTTACAGAGAGAGAGAGAGAGAGAGAG 705
 |||||
 QY 691 AACTCAGCGAGTCAATCGGCGCACTTACCGGAGTCTCTTCCAGAGCAGAGAGAGAG 749
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 DB 706 AACTCAGCGAGTCAATCGGCGCACTTACCGGAGTCTCTTCCAGAGCAGAGAGAGAGAG 764
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RESULT 7
 US-09-621-976-2162
 ; Sequence 2162, Application US/09621976
 ; Patent No. 6639063
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, J.B.
 ; APPLICANT: Jober, S.
 ; APPLICANT: Giordano, J.Y.
 ; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
 ; FILE REFERENCE: GENSET.054PR2
 ; CURRENT APPLICATION NUMBER: US/09/621,976
 ; CURRENT FILING DATE: 2000-07-21
 ; NUMBER OF SEQ ID NOS: 19335
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 2162
 ; LENGTH: 391
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 17..223
 ; US-09-621-976-2162

Query Match 10.5%; Score 90.4; DB 3; Length 391;
 Best Local Similarity 75.7%; Pred. No. 6.3e-11;
 Matches 112; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

607 GGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 666
 |||||
 DB 26 GGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 85
 |||||
 QY 667 GGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 726
 |||||
 DB 86 GGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 145
 |||||
 QY 727 TCTTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 754
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 DB 146 TCTTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 173
 |||||

RESULT 8
 US-09-902-540-6620
 ; Sequence 6620, Application US/09902540
 ; Patent No. 6833447
 ; GENERAL INFORMATION:
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Wiegand, Roger C.
 ; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
 ; FILE REFERENCE: 38-10(15849)B
 ; CURRENT APPLICATION NUMBER: US/09/902,540
 ; CURRENT FILING DATE: 2001-07-10
 ; PRIOR APPLICATION NUMBER: 60/217,883

;; PRIOR FILING DATE: 2000-07-10
;; NUMBER OF SEQ ID NOS: 16825
;; SEQ ID NO 6620
;; LENGTH: 645
;; TYPE: DNA
;; ORGANISM: Myxococcus xanthus
US-09-902-540-6620

Query Match 6.6%; Score 57.2; DB 3; Length 645;
Best Local Similarity 45.7%; Pred. No. 0.0016;
Matches 200; Conservative 0; Mismatches 238; Indels 0; Gaps 0;

QY 236 TGTGAGGACAGGATCCCAAGAGCCGCAAGTCTACGCCCCGCTCGGCCCAACGACCGCC 355
DB 80 TGGCGGAGACGGCGCATCTCGAAGTGTGAAGAGAACCCCTTCTGTCACTTCTTACA 139
QY 356 TGGCGGTGCGCCCTTTCGCCAGCGGAGCGCTTCCACCGCTTCCAGCCCACTATCCGT 415
DB 140 CGGACCGGAGAAAGTTCCGCTTCCAGAGCATCTTCTTCTGCTGTGCGCTTCCGTC 199
QY 416 ACTTGACAGCAGATGCACTTGCACTTCCACCACTTCTGTCAGACGGGAGAGCCCC 475
DB 200 AGCAGCAGAGAGCTTCCAGAGGAACTTCTGAGCTGATGACGGTCAAGCAGACTACTGT 259
QY 476 CACCTTACAGAGGCCCCCTGACCTTCCAGCTTCCGAGCCGAGAGCAGCTGGAATGA 535
DB 260 TCGCCAGAGACCGCATCTTTCGCGCATCACTTGACGCGACGAGCTGCGCTTCTTACG 319
QY 536 ACCGGAGTGTGTCGCGCAGACCCCAAGAGAACATCTTTCAGAGTGAAGTGAATGA 595
DB 320 AGCGGTCTTTCAGAGGCTGCGGCGCCCGGCTGAGCGGACCTGTCTATCTACTCC 379
QY 596 GTGCCAGGTGAGCGGCGCCCTTCCGCCCAAGTAATCTGGGATCAGCGCAAGTGT 655
DB 380 AGGCCGAGTGAAGCTGCTCTGCAACCGCATCAAGAGCGCGCGGAGTTTGAAGCGCA 439
QY 656 AGCGCAGCGCGGCGGATGAGAGGCGCGCCGCCCACTTCAAGCGAGTCACTCGGCACT 715
DB 440 AGTTGACCCCAAGTACTGAGAGGCGCTGTCATCTTCAACAACATCTTCTTCTCACT 499
QY 716 ACCCGGGTCTCTCTCC 733
DB 500 ACACGAGACCCCGCTCC 517

RESULT 9
US-09-902-540-506
; Sequence 506, Application US/09902540
; Patent No. 6833447

;; GENERAL INFORMATION:
;; APPLICANT: Goldman, Barry S.
;; APPLICANT: Hinkle, Gregory J.
;; APPLICANT: Slater, Steven C.
;; APPLICANT: Wiegand, Roger C.
;; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;; FILE REFERENCE: 38-10(15849)B
;; CURRENT APPLICATION NUMBER: US/09/902,540
;; PRIOR FILING DATE: 2001-07-10
;; PRIOR APPLICATION NUMBER: 60/217,883
;; PRIOR FILING DATE: 2000-07-10
;; NUMBER OF SEQ ID NOS: 16825
;; SEQ ID NO 506
;; LENGTH: 2364
;; TYPE: DNA
;; ORGANISM: Myxococcus xanthus
US-09-902-540-506

Query Match 6.6%; Score 57.2; DB 3; Length 2364;
Best Local Similarity 45.7%; Pred. No. 0.0022;
Matches 200; Conservative 0; Mismatches 238; Indels 0; Gaps 0;

QY 296 TGTGAGGACAGGATCCCAAGAGCCGCAAGTCTTACGCCCCGCTCGGCCCAACGACCGCC 355
DB 111 TGTGAGGACAGGATCCCAAGAGCCGCAAGTCTTACGCCCCGCTCGGCCCAACGACCGCC 355

DB 734 TGGCGGAGACGGCGCATCTCGAAGTGTGAAGAGAACCCCTTCTGTCTGCACTTCTACA 793
QY 356 TGGCGGTGCGCCCTTTCGCCAGCGGAGCGCTTCCACCGCTTCCAGCCCACTATCCGT 415
DB 794 CGGACCGGAGAAAGTTCCGCTTCCAGAGCATCTTCTTCTGCTGTGCGCTTCCGTC 853
QY 416 ACTTGACAGCAGATGCACTTGCACTTCCACCACTTCTGTCAGACGGGAGAGCCCC 475
DB 854 AGCAGCAGAGAGCTTTCAGAGGAACTTCTGAGCTGATGACGGTCAAGCAGACTACTGT 913
QY 476 CACCTTACAGAGGCCCCCTGACCTTCCAGCTTCCGAGCCCGAGAGCAGCTGGAATGA 535
DB 914 TCGCAGAGAACGATCTTTCGCGCATCTTCAACTTGAAGCGGCAAGAGCTGCGCTTACG 973
QY 536 ACCGGAGTGTGTCGCGCAGACCCCAAGAGAACATCTTTCAGAGTGAAGTGAATGA 595
DB 974 AGCGGTCTTTCAGAGGCGCTGCGGCGCCCGTGGCCAGACCGGACCTGTCTATCTACTCC 1033
QY 596 GTGCCAGGTGAGCGGCGCCCTTTCGCCCAAGTAATCTGGGATCAGCGCCAGCTGT 655
DB 1034 AGGCCGAGTGAAGCTGCTCTGCAACCGCATCAAGAGCGCGCGGAGTTTGAAGCGCA 1093
QY 656 AGCGCAGCGCGGCGGATGAGAGGCGCGCCGCCCACTTACAGCGAGTCACTGCGCACT 715
DB 1094 AGTTGACCCCAAGTACTGAGAGGCGCTGTCATCTTCAACAACATCTTCTTCTCACT 1153
QY 716 ACCCGGGTCTCTCTCC 733
DB 1154 ACACGAGACCCCGCTCC 1171

RESULT 10
US-09-902-540-904
; Sequence 904, Application US/09902540
; Patent No. 6833447
;; GENERAL INFORMATION:
;; APPLICANT: Goldman, Barry S.
;; APPLICANT: Hinkle, Gregory J.
;; APPLICANT: Slater, Steven C.
;; APPLICANT: Wiegand, Roger C.
;; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;; FILE REFERENCE: 38-10(15849)B
;; CURRENT APPLICATION NUMBER: US/09/902,540
;; PRIOR FILING DATE: 2001-07-10
;; PRIOR APPLICATION NUMBER: 60/217,883
;; PRIOR FILING DATE: 2000-07-10
;; NUMBER OF SEQ ID NOS: 16825
;; SEQ ID NO 904
;; LENGTH: 11382
;; TYPE: DNA
;; ORGANISM: Myxococcus xanthus
US-09-902-540-904

Query Match 6.2%; Score 53.2; DB 3; Length 11382;
Best Local Similarity 47.4%; Pred. No. 0.024;
Matches 259; Conservative 0; Mismatches 278; Indels 9; Gaps 3;

QY 234 GGGCGGAGAGAGAAAGATGCCCTGTCTCAGAAAGATGCTGTGGCCCTCGAAGACAC 293
DB 920 GCGCGGTGGAATGAAGCCCTGCTCATGACCGGGGCAACCCGACGATGAGGAGGAA 979
QY 294 AGTGTACAGCAAGCAATCCAGAGCCGAGGCTTACAGCCCGCGCTCGGCCCAACGACCG 353
DB 980 CGGCTCTTCACCCGAGACCTGTAGCCGCGGAGAGACCAACCAAGCGGCCACCTGT 1039
QY 354 CCTGCGGTGCGCCCTTTCGCCAGCGGAGCGCTTCCACCGCTTCCAGCCCACTATCC 413
DB 1040 CCAAGCCCAAGCGCGGCCCAAGCGGTGACGCTGTGATGAGAGAGAGCC-----GTTC 1095
QY 414 GTACTGACAGCAGAGTGAAGCTTGCACCACTTCTGCTGTGAGAGGGAGAGAGCC 473
DB 1096 CGGATGAAGCGCGGAGAAACCAAGCAGTAGACGTTCAGCGCCCGCATCAGAGAGAGCC 1155

QY 474 CCCACCTTACCGAGGCCCCCTTCAC--CCTCAGCTTGGGAGCCCCGAGCAGACTGGA 530
DB 1156 ACGCCCCACGACGCGAGTGCCCTTGGGCTCTGCTTCAGGCGCGGAGCAGACAGGA 1215
QY 531 ACTGAACCGGAGTGTGTGCGGACCCCCAAGAACATCTTTCAGAGTACTGAT 590
DB 1216 A--GAACGCGACGAGAGTGTGCCCCAGCGCAGACACCGCAGCCGAGCAGCC 1273
QY 591 GGATAGTGCAGAGTGTGCGGCGCCCTGCCCCCAGCAGTAACTGCGGATCAGCGCAC 650
DB 1274 GTTCGAGGCGCGCGCGGTACCACTGTCCTCTCGGAAGCGAGCATCATCAGCAG 1333
QY 651 GTGCTACGCGACGCGCGCGCGCATGAGGCGCGCGCCCTTACAGTACGAGTCTCG 710
DB 1334 GAGCTGCGAGAGCGCGCGGTACGCCCAAGCAGAGAGCGAGCAGGAGTCCCCAG 1393
QY 711 CCACTACCGCGGCTCTCTCTTCAGAGACAGAGCAGAGTGGCGCGCTCTGCTGGA 770
DB 1394 CGGAGGAAAGTGTGCGGTCCATCAACGCGCGGAATGTCTCCGCGCGCGCGTGC 1453
QY 771 GGGGAC 776
DB 1454 CGCGAC 1459

RESULT 11

US-09-902-540-8567/c
Sequence 8567, Application US/0902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 8567
LENGTH: 1884
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-8567

Query Match 6.1%; Score 52.6; DB 3; Length 1884;
Best Local Similarity 48.0%; Pred. No. 0.022;
Matches 213; Conservative 0; Mismatches 226; Indels 5; Gaps 2;

QY 336 GCGTGGGCGCACGACCGGCTGGCGGCGCCCTTTCGCGGAGGCGCTTCCACG 395
DB 1810 GCGGCGACGCGCGCGCGCTTCAGCGCCCAACGCGGCTCCAGCGGTACCTGTGC 1751
QY 396 CTTCACGCCCACTTATCTGCTTACCTGACGACGAGATGACCTTCCACCACTTCGCT 455
DB 1750 AGTGAACGACGCGCGCTCCGAGTGAAGCGCGGGAACAACAGCAGTACGCTCCAGCG 1691
QY 456 GTCAAGCGGAGAGAGCCCCACCTTACGAGGCGCTTCGAC--CCTCAGTTTGGGA 512
DB 1690 CCGGCAATCAGAGCAGCAGCGCCCAAGCGGCGAGTGCCTTGGTCTCTGCTTCAGGC 1631
QY 513 CCGGAGCAGCAGTGAATGAACCGGAGTGTGTCGCGCACCCCAAGAACAT 572
DB 1630 GCGGAGCAGCAGGAA--GAACGACAGAGAGTGTCCACGCGCAGACACCGC 1573
QY 573 CTTCGACGTCAGCTGATGATGATGTCAGGCTGGGCGGCGCTTCGCGCAGAGTAA 632
DB 1572 CACCGGAGCGACGACGCTGAGGCGCGCGGTACCACTGTCCTTCGGAAGCGA 1513
QY 633 CTGGGATCATGCGCGCAGTGTCTTACGAGCGGCGGCGCATGAGAGGCGCGCGCCAC 692

DB 1512 CGCATTCATATCAGCAGAGTGTGAGAGAGCGCGGTACGCCCAAGCAGACGAAAGC 1453
QY 693 CTACAGCAGAGTCAATCGGCACTACCGGCGTCTCTTCCAGACACGAGAGAGTGG 752
DB 1452 GAGCAGCAGGATCTCCCAACCCGAGAGAGTGTGCGCGGTCCATCAACGCGCACTGTCC 1393
QY 753 GCGGCGCTCTTGTGTGAGGAGGAC 776
DB 1392 CGCGCGCGCGCGCGTGGCGCGGAC 1369

RESULT 12

US-10-104-047-1064
Sequence 1064, Application US/10104047
Patent No. 6943241
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. 6943241el full1 length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1064
LENGTH: 2183
TYPE: DNA
ORGANISM: Homo sapiens
US-10-104-047-1064

Query Match 5.9%; Score 51; DB 3; Length 2183;
Best Local Similarity 46.8%; Pred. No. 0.051;
Matches 227; Conservative 0; Mismatches 255; Indels 3; Gaps 2;

QY 313 CCAGAGCGCAGAGTCAACGCGCCCTGCGCCCAAGCGCGCTGCGCGCTTC 372
DB 593 CACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 652
QY 373 GCCAGCGGAGCGCTTCCAGCGCTTCCAGCCCACTTCTGCTGACGACGAGATC 432
DB 653 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 712
QY 433 GACCTGACCAACCATCTGCTGTCAAGCGGAGAGAGCCCACTTACAGAGGCGCC 492
DB 713 CCGCAGCAGTACTTCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 772
QY 493 TGCACCTTCAGCTTGGGAGCCCGGACGACGAGCTGAACTGAACCGGAGTGTGC-G 551
DB 773 TACAGCTTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 832
QY 612 CCCCTGCCCCCAGCAGTAACTCGGCGCATCAGCGCACTGTGTAGAGCGCGGCG 671
DB 893 CAGCAGCCCAAGTGAAGAACAGCAGCGCCCACTGATGACAGCAGCGCCCACTGAC 952
QY 672 CATGAGGAGCGCGCGCCCACTTACAGAGGTCATCGGCACTACCGGAGTCTTC-- 729
DB 953 CAGCAGAGCCCAAGCCCGCTGAGCAGCAGCCCACTGACAGCAGCAGCAGCAG 1012
QY 730 TTCAGACACAGCAGAGAGTGGCGCGCTCTCTTCTGAGAGGAGACCGGCTTCACAC 789
DB 1013 TCCACACACAGCAGATGCCAGCAGCAGAGTCCCAAGCAGCAGCGCCCAAGCAGCTG 1072
QY 790 ACACA 794
DB 1073 CCGCA 1077

RESULT 13

US-09-949-016-3915
; Sequence 3915, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3915
; LENGTH: 1122
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3915

Query Match
Best Local Similarity 47.7%; Score 50.2; DB 3; Length 1122;
Matches 179; Conservative 0; Mismatches 193; Indels 3; Gaps 1;

QY 323 AGGTCTACGCCCCCGCTCGCCGACCGACCGCTGGCCGCTTCCGCCACGGG 382
DB 306 AGTTGCCCCCTGTGCCCCGGGAGACCCCGGCGCCAGCTGCGCAAGTACGGCTGC 365
QY 383 AGCGCTTCACCGCTTCCAGCCCACTTATCCGTACTGACGACGAGATGCACTGCCAC 442
DB 366 CGGGGCTGGCGAGCTCAAGACCGCGAGTCCGTAAGTGTGCTA---CGACCGCGCA 422
QY 443 CCACCATCTCGCTGTACAGACGGGAGAGCCCCACCCACCAAGGGCCCCCTGACCCCTCC 502
DB 423 CCGCGCGCGCTCTGAGGTGAGAGCACTGACCCGACCGGTCTCCCGCGGAGAGGGG 482
QY 503 AGCTTCGGGAGCCCGGACGAGCTGAACTGAACCGGAGTGTGCGGACCCCA 562
DB 483 ACCGGCGGAGTGGCACTTCCGAGAGAGCACTCGGTGACGCTACACCGTGCACACA 542
QY 563 ACAGAACCATCTTGCAGACTGACTGATGATAGTCCAGGCTGGGGCCCTGCTGCC 622
DB 543 AGCGGCACTACCGCGGCACTGGCTTGCACCGCGGTCACTTGGCGCGCGCCCAACACC 602
QY 623 CCAGCAGTAACTCGGGCATCAGCGGCACTGCTTACCGGACGGCGGGCCCATGAGGGGC 682
DB 603 GCTGAGCCAGAAAGCCATGAGCAGACGTTCTTACTGAGCAAGTCCGCGCCCAAGTGC 662
QY 683 CGCCGCCACCTACA 697
DB 663 CCCACTCAACAGA 677

RESULT 14
US-09-252-991A-13687
; Sequence 13687, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27.
; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 13687
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13687

Query Match
Best Local Similarity 57.2%; Score 48; DB 3; Length 696;
Matches 87; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 109 ACGAGCTGAGATTGTTCAGATCATCATCTGTTGTTGATGATGATGATGATG 168
DB 482 ACCCTGTAATCTTCTGTTGGCATGTCGCGCGGGGTGTCCTGGCGGTGCTG 541
QY 169 GTGATCAGTCTGCTGCTGAGCACTACAAAGCTGTGACGCTCTTATCAGCCGGAC 228
DB 542 CTGATCAAGCGCTGCTGCTGCGAAGAAAGAAAGCTGAGCTGACCTGACCTGCGGAG 601
QY 229 AGCCAGGGCGGAGAGAGAGATGCCCTGTC 260
DB 602 CGCATTCGCGAGGCGGAGATGCGCCCTGCG 633

RESULT 15
US-09-252-991A-13650/C
; Sequence 13650, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13650
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13650

Query Match
Best Local Similarity 57.2%; Score 48; DB 3; Length 1452;
Matches 87; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 109 ACGAGCTGAGATTGTTCAGATCATCATCTGTTGTTGATGATGATGATGATG 168
DB 267 ACCCTGTAATCTTCTGTTGGCATGTCGCGCGGGGTGTCCTGGCGGTGCTG 208
QY 169 GTGATCAGTCTGCTGCTGAGCACTACAAAGCTGTGACGCTCTTATCAGCCGGAC 228
DB 207 CTGATCAAGCGCTGCTGCTGCGAAGAAAGAAAGCTGAGCTGACCTGACCTGCGGAG 148
QY 229 AGCCAGGGCGGAGAGAGAGATGCCCTGTC 260
DB 147 CGCATTCGCGAGGCGGAGATGCGCCCTGCG 116

Search completed: February 28, 2006, 12:29:27
Job time : 176.41 secs

	661	721	781	841
Db	AGCGGCGGCGCATGAGGGGCGCGCCACCTACAGCGAGGTCAATCGGCACCTACCG			
Qy	GGGTCCTCTTTCAGACCCAGACGAGCAAGTGGCGCGCCTCTTGTGTGAGGGGACCCGG			
Db	GGGTCTCTTTCAGAGACCAAGACAGCAAGTGGGGCGCCTCTTGTGTGAGGGGAGCCCGG			
Qy	CTCCACCAACACACATCATCGCGCCCTTAAAGAGGGCGGCGCATCTTGAGCAAAAGGAAGGAT			
Db	CTCCACCAACACACATCATCGCGCCCTTAAAGAGGCGGCGCATCTTGAGCAAAAGGAAGGAT			
Qy	AAACGAAAGGACACCCCTCTC	861		
Db	AAACGAAAGGACACCCCTCTC	861		

RESULT 3

```

US-09-934-249-1
Sequence 1, Application US/09934249
Patent No. US20020115081A1
GENERAL INFORMATION:
APPLICANT: Lee, Richard T.
APPLICANT: Landeschilz, Katherine T.
APPLICANT: Tuft, Thomas G.
APPLICANT: Thompson, John F.
APPLICANT: Kennedy, Scott P.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
FILE REFERENCE: P0738/7001/ERP/KA
CURRENT APPLICATION NUMBER: US/09/934,249
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FaastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1321
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (413)...(1273)
US-09-934-249-1

```

Query Match	100.0%;	Score 861;	DB 3;	length 1321;
Best Local Similarity	100.0%;	Pred. No. 1.6e-219;		
Matches 861;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	ATGCAACCGGTTATATGGGGGGTCAACACACACCGCCGCGCGCGCGCGCGAGGCCAATATGTC	60
Db	413	ATGCACCGCTTATATGGGGGGTCAACACACACCGCCGCGCGCGCGCGCGAGGCCAATATGTC	472
QY	61	TCTGCAACGTGCAAACTGCAAACGCTCTTTGTTCACAGACATGGAGATCAACGAGCTGGAG	120
Db	473	TCTGCAACGTGCAAACTGCAAACGCTCTTTGTTCACAGACATGGAGATCAACGAGCTGGAG	532
QY	121	TTTGTTCAGATCATCATATCGTGTGTGTGTATATGTATATGGTGTGTGTATCATAGTGC	180
Db	533	TTTGTTCAGATCATCATATCGTGTGTGTGTATATGTATATGGTGTGTGTATCATAGTGC	592
QY	181	CTGTGAGGCACATACAAAGCTGTCTGCACGGTCTTATATCAGCCGGACACAGCCAGGGGCGG	240
Db	593	CTGTGAGGCACATACAAAGCTGTCTGCACGGTCTTATATCAGCCGGACACAGCCAGGGGCGG	652
QY	241	AGGAGAGAAATGTCCTGTCTCTCAAGAAAGATGCTGTGTGTGTGTCTGTGTGTGTGTGTCA	300
Db	653	AGGAGAGAAATGTCCTGTCTCTCAAGAAAGATGCTGTGTGTGTGTCTGTGTGTGTGTGTCA	712
QY	301	GGCAACGGAATCCCAAGACCGCAGAGTATAGCCCGCGCTGAGCCCAACCGACCGCTGGCC	360
Db	713	GGCAACGGAATCCCAAGACCGCAGAGTATAGCCCGCGCTGAGCCCAACCGACCGCTGGCC	772
QY	361	GTGCGCGCTCTGTGCGCCAGCGGAGCGCTTCAACCGCTTCAAGCCCACTATCCGTACTG	420

Db	773	GTGCGCCCTTCGCGCCACAGCGGAGCGGTTCCACCGCTTCCAGGCCACCTAACGTA	CTG	832			
QY	421	CAGCAGCAGATCGACCTTGCCA	CCCCACATCTCGCTGTCAACGCGGAGAGAGCC	CCCCCACC	480		
Db	833	CAGCAGCAGATCGACCTTGCCA	CCCCACATCTCGCTGTCAACGCGGAGAGAGCC	CCCCCACC	892		
QY	481	TACCAAGGAGCCCTTCACCCCTTCAGCTTCGGAGCCCCAGCAGCAGCTGGA	ACTGGA	CCGG	540		
Db	893	TACCAAGGAGCCCTTCACCCCTTCAGCTTCGGAGCCCCAGCAGCAGCTGGA	ACTGGA	CCGG	952		
QY	541	GAGTCGGTGGCGGACCCCTCCAA	CAGAACCATCTTTCGACAGTGA	CTGATGGA	TATGTC	600	
Db	953	GAGTCGGTGGCGGACCCCTCCAA	CAGAACCATCTTTCGACAGTGA	CTGATGGA	TATGTC	1012	
QY	601	AGGCTGGGCGGCGCCCTGTC	CCCCCGCAGAGATTA	CTCGGGCATCAGCGC	CACTGCTCA	CGGC	660
Db	1013	AGGCTGGGCGGCGCCCTGTC	CCCCCGCAGAGATTA	CTCGGGCATCAGCGC	CACTGCTCA	CGGC	1072
QY	661	AGCGGCGGCGCATGAGAGGGCGCG	CGCCCACTACAGCGAGTCA	TGCGCACTA	CCCG		720
Db	1073	AGCGGCGGCGCATGAGAGGGCGCG	CGCCCACTACAGCGAGTCA	TGCGCACTA	CCCG		1132
QY	721	GGGTCTCTCTTCAGACAC	CAGCAGAGCAGTGGCGCG	CGCTCTTGTGTA	GGGAC	CCCG	780
Db	1133	GGGTCTCTCTTCAGACAC	CAGCAGAGCAGTGGCGCG	CGCTCTTGTGTA	GGGAC	CCCG	1192
QY	781	CTCCACCA	CACACATTCGCGCGCCCTTGAGAGCG	CAGCATCTTGAG	CTAAAGAGAA	GGAT	840
Db	1193	CTCCACCA	CACACATTCGCGCGCCCTTGAGAGCG	CAGCATCTTGAG	CTAAAGAGAA	GGAT	1252
QY	841	AAACGAAAGGACACCTCTC	861				
Db	1253	AAACGAAAGGACACCTCTC	1273				

RESULT 4

```

US-10-241-220-119
Sequence 119, Application US/10241220
Publication No. US20030148408A1
GENERAL INFORMATION:
APPLICANT: Franz, Gretchen
APPLICANT: Hillan, Kenneth J.
APPLICANT: Phillips, Heidi
APPLICANT: Polakis, Paul
APPLICANT: Spencer, Susan
APPLICANT: Williams, P. Mickey
APPLICANT: Wu, Thomas
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TREATMENT OF TUMOR
FILE REFERENCE: P5010R1-US
CURRENT APPLICATION NUMBER: US/10/241,220
CURRENT FILING DATE: 2002-12-13
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 119
LENGTH: 4839
TYPE: DNA
ORGANISM: Homo Sapien
US-10-241-220-119

```

Query Match	100.0%;	Score 861;	DB 6;	Length 4839;
Best Local Similarity	100.0%;	Pred. No. 1.9e-219;		
Matches 861;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

[illegible]


```

? GENERAL INFORMATION:
? APPLICANT: HRUBAN, RALPH H.
? APPLICANT: ARGANI, PEGRAM
? APPLICANT: IACOBUZIO-DONNAUE, CHRISTINE
? APPLICANT: MAITRA, ANIRBAN
? TITLE OF INVENTION: PANCREATIC CANCER DIAGNOSIS AND THERAPIES
? FILE REFERENCE: 58303(71699)
? CURRENT APPLICATION NUMBER: US/10/269,909
? CURRENT FILING DATE: 2003-10-11
? PRIOR APPLICATION NUMBER: 60/328,609
? PRIOR FILING DATE: 2001-10-11
? PRIOR APPLICATION NUMBER: 60/332,754
? PRIOR FILING DATE: 2001-11-19
? NUMBER OF SEQ ID NOS: 87
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 85
? LENGTH: 4839
? TYPE: DNA
? ORGANISM: Homo sapiens
US-10-269-909-85

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Query Match	100.0%;	Score 861;	DB 6;	Length 4839;
Best Local Similarity	100.0%;	Pred. No. 1.9e-219;		
Matches 861;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

Accession	Sequence	Length
QY	GGGTCCTCTTTCAGACACAGAAAGAGTGTGAGCGCCCTCTTGTGTGAAGGACCCGG	780
Db	GGGTCCTCTTTCAGACACAGAAAGAGTGTGAGCGCCCTCTTGTGTGAAGGACCCGG	11041
QY	CTCCACCAACACACATATCGCGCCCTTAGAGAGCGCAGCCATCTGTGAGCAAGAGAGAT	840
Db	CTCCACCAACACACATATCGCGCCCTTAGAGAGCGCAGCCATCTGTGAGCAAGAGAGAT	1101
QY	AAACAGAAAGACACCTCTC	861
Db	AAACAGAAAGACACCTCTC	1161

RESULT 7

US-10-872-972-119
; Sequence 119, Application US/10872972
; Publication No. US20040229277A1
; Publication No. US20040229277A1

GENERAL INFORMATION:

APPLICANT: Frantz, Gretchen
; APPLICANT: Hilian, Kenneth J.
;

APPLICANT: phillips, Heidi
APPLICANT: polakis, Paul

APPLICANT: Spencer, Susan
APPLICANT: Williams, P. Mickey

```

; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zhenli
; SUBJECT: INVENTION CONCEPTS AND METHODS FOR THE DIAGNOSIS AND

```

```
; TITLE OF INVENTION: COMPOSITIONS AND METHODS  
; TREATMENT OF TUMOR  
; TITLE OF INVENTION: TREATMENT OF TUMOR
```

```

; FILE REFERENCE: P5010R1-US
; CURRENT APPLICATION NUMBER: US/10/872,972
; CURRENT FILING DATE: 2004-06-21

```

```

; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US/10/241,220
; PRIOR FILING DATE: 2003-06-11

```

; PRIOR FILING DATE: 2002-0
 ; NUMBER OF SEQ ID NOS: 120

```

; SEQ ID NO 119
; LENGTH: 4839
;

```

Query Match	100.0%	Score 861;	DB 8;	Length 4839;
Best Local Similarity	100.0%;	Pred. No. 1.9e-219;		
Matches 861; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0.

QY	I	ATGCACCGCTTGATGAGGGGTCAACAGCACCGCCGGCGCGCGCGGGGACGGCCAAATGTC	60
Db	321	ATGCACCGCTTGATGAGGGGTCAACAGCACCGCCGGCGCGCGGGGACGGCCAAATGTC	380
QY	61	TTCCGCAAGTGCACCTGCAAACGCTTGTGTTCCAGACATGGAATCAAGAGCTGAG	120
Db	381	TTCCGCAAGTGCACCTGCAAACGCTTGTGTTCCAGACATGGAATCAAGAGCTGAG	440
QY	121	TTTGTTCAGATCATCATCATCGTGGTGTGATGATGATGATGATGATGATGATGATCA	180
Db	441	TTTGTTCAGATCATCATCATCGTGGTGTGATGATGATGATGATGATGATGATGATCA	500
QY	181	CTGCTGAGCCACTACAGACTGTCTGCAAGCTTCCTTATCAGCCGAGCACAGCCAGGGCGG	240
Db	501	CTGCTGAGCCACTACAGACTGTCTGCAAGCTTCCTTATCAGCCGAGCACAGCCAGGGCGG	560
QY	241	AGGAGAGAAGATGCCCTGTCTCAGAGAGATCCTGTGGCCCTCGAGAGCACAGTGTCA	300
Db	561	AGGAGAGAAGATGCCCTGTCTCAGAGAGATCCTGTGGCCCTCGAGAGCACAGTGTCA	620
QY	301	GCGCAACGAAATCCAGAGCCGAGGTCTACGCCGCCGCTCGGCCACAGCAGCGCTGTGGCC	360
Db	621	GCGCAACGAAATCCAGAGCCGAGGTCTACGCCGCCGCTCGGCCACAGCAGCGCTGTGGCC	680
QY	361	GTCGCCGCTTTGCGCCAGCGGAGGGCTTCCAGCCGCTTCCAGGCCACCTATCCGTAACCTG	420
Db	681	GTCGCCGCTTTGCGCCAGCGGAGGGCTTCCAGCCGCTTCCAGGCCACCTATCCGTAACCTG	740
QY	421	CAGCACAGAGATGACCTTGCCACCCACATCTTCGTGTCAAGACGGGGAAGAGGCCCCACACC	480

Db	741	CAGCAGAGATGACCTTGTGACCAACCACTTGTGTGTGAGACGGGGAGAGAGCCCCCAACC	800
Qy	481	TACCAAGGGCCCCCTGCAACCCCTCAGCTTGGGAGACCCGAGACAGCACTGAACTGAACCGG	540
Db	801	TACCAAGGGCCCCCTGCAACCCCTCAGCTTGGGAGACCCGAGACAGCACTGAACTGAACCGG	860
Qy	541	GAGTGGGTGGCGGCACCCCCCAACAGAACCATCTTTCAGCAGTGCACCTGATGTGATGTGCC	600
Db	861	GAGTGGGTGGCGGCACCCCCCAACAGAACCATCTTTCAGCAGTGCACCTGATGTGATGTGCC	920
Qy	601	AGGCTGGGGCGGCCCTTGCCCCCGCCAGCAGTAACCTGGGCATCAGGCGCAGCGTACAGGCG	660
Db	921	AGGCTGGGGCGGCCCTTGCCCCCGCCAGCAGTAACCTGGGCATCAGGCGCAGCGTACAGGCG	980
Qy	661	AGCGCGGGCGCATATGAGAGGGCGCGCGCCACTTACAGCGAGGTATCTGCGCCACTTACCGG	720
Db	981	AGCGCGGGCGCATATGAGAGGGCGCGCGCCACTTACAGCGAGGTATCTGCGCCACTTACCGG	1040
Qy	721	GGGTCTCTCTTTCAGCACACAGCAGAGCAGTGGGCGGCCCTCTCTTGTGAGAGGGACCCGG	780
Db	1041	GGGTCTCTCTTTCAGCACACAGCAGAGCAGTGGGCGGCCCTCTCTTGTGAGAGGGACCCGG	1100
Qy	781	CTCCACCAACAACAATGCGCGCCCTTAAGAGAGCGCAGCATTGTGAGCAAAAGAAAGGAT	840
Db	1101	CTCCACCAACAACAATGCGCGCCCTTAAGAGAGCGCAGCATTGTGAGCAAAAGAAAGGAT	1160
Qy	841	AAACAGAAAGCACCCCTCTC	861
Db	1161	AAACAGAAAGCACCCCTCTC	1181

RESULT 8

; Sequence 119, Application US/10872991
; Publication No. US20040242860A1

```

1  APPLICANT:  Frantz,Gretchen
2  APPLICANT:  Hillan,Kenneth J.
3  APPLICANT:  Phillips, Heidi
4  APPLICANT:  Polakis,Paul
5  APPLICANT:  Spencer,Susan
6  APPLICANT:  Williams,P. Mickey
7  APPLICANT:  Wu,Thomas
8  APPLICANT:  Zhang,Zemin
9  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
10 TITLE OF INVENTION: TREATMENT OF TUMOR
11 PIR REFERENCE:  P501031-US
12 CURRENT APPLICATION NUMBER:  US/10/872,991
13 CURRENT FILING DATE:  2004-06-21
14 PRIOR APPLICATION NUMBER:  US/10/241,220
15 PRIOR FILING DATE:  2002-09-11
16 NUMBER OF SEQ ID NOS:  120
17 SEQ ID NO 119
18 LENGTH:  4839
19
20 TYPE:  DNA
21 ORGANISM:  Homo Sapien
22 US-10-872-991-119

```

Query Match	100.0%	Score 861, DB 8	Length 4839
Best Local Similarity	100.0%	Pred. NO. 1.9e-219	
Matches 861, Conservative	0	Mismatches 0	Gaps 0

[illegible]

D	b	441	TTTTGTTCAGATTCATCATCATCATCTGTGTGTGTATGATGTGATGTGTGTGTATCATCTGTC	500
O	y	181	CTGTGTAGCCACTTACAAAGCTGTCTGTGCACGGTCTCTTATCAAGCCGGGCACAGCCAGAGGGCCGG	240
D	b	501	CTGTGTAGCCACTTACAAAGCTGTCTGTGCACGGTCTCTTATCAAGCCGGGCACAGCCAGAGGGCCGG	560
O	y	241	AGGAGAGAGATGTCCTGTCTCTTCAGAAAGGATGTCTGTGTGGCCCTGTGGAGAGACAGTGTCA	300
D	b	561	AGGAGAGAGATGTCTCTGTCTCTTCAGAAAGATGTCTGTGTGGCCCTGTGGAGAGACAGTGTCA	620
O	y	301	GGCAACGGAAATCCAGAGCCGCAGAGTCTACGCCGCCCTCGGACCCACGACGACCGCTGACC	360
D	b	621	GGCAACGGAAATCCAGAGCCGCAGAGTCTACGCCGCCGCCCTCGGACCCACGACCGCTGACC	680
O	y	361	GTGTCGCCCTTTCGCCCAAGCCGGAGCGCTTCCACCGCTTCCAGGCCACCTTATCGTACTGT	420
D	b	681	GTGTCGCCCTTTCGCCCAAGCCGGAGCGCTTCCACCGCTTCCAGGCCACCTTATCGTACTGT	740
O	y	421	CAGACACGAGATTCGACCTGTGCACCCACCATCTCGTGTGTACAGCCGGGAGAGAGCCGCCACC	480
D	b	741	CAGACACGAGATTCGACCTGTGCACCCACCATCTCGTGTGTACAGCCGGGAGAGAGCCGCCACC	800
O	y	481	TACCAAGGAGCCCTTGCACACCTTCAAGCTTTCGGGACCCGACAGCAGCTGTGAACCTGAACCGG	540
D	b	801	TACCAAGGAGCCCTTGCACACCTTCAAGCTTTCGGGACCCGACAGCAGCTGTGAACCTGAACCGG	860
O	y	541	GAGTCGGGTGCGGACCCGCCAAGAAACCATCTTTCGACAGTGAACCTGATGATGTATGTCC	600
D	b	861	GAGTCGGGTGCGGACCCGCCAAGAAACCATCTTTCGACAGTGAACCTGATGATGTATGTCC	920
O	y	601	AGGCTGTGGGGGGCCCCCTGTGCCCCCGACAGATTAATCTCGGGCAATCAACGGCAGGTGTAAAGGGC	660
D	b	921	AGGCTGTGGGGGGCCCCCTGTGCCCCCGACAGATTAATCTCGGGCAATCAACGGCAGGTGTAAAGGGC	980
O	y	661	AGCGGCGGGGCGCATGTGAGAGGGGCGCGCGGCCACTTACAGCGAGTCTATCGGSCACTAACCGG	720
D	b	981	AGCGGCGGGGCGCATGTGAGAGGGGCGCGCGGCCACTTACAGCGAGTCTATCGGSCACTAACCGG	1040
O	y	721	GGGTCTCTCTTTCAGACACCAAGCAGAGCATGTGTGGCGCGCTCTTGTGTGAGGGGACCCGG	780
D	b	1041	GGGTCTCTCTTTCAGACACCAAGCAGAGCATGTGTGGCGCGCTCTTGTGTGAGGGGACCCGG	1100
O	y	781	CTTCAACCAACACATTCGGCGCCCTTGAAGAGCGCAGCATCTGTGAGCAAAAGAGAGAT	840
D	b	1101	CTTCAACCAACACATTCGGCGCCCTTGAAGAGCGCAGCATCTGTGAGCAAAAGAGAGAT	1160
O	y	841	AAACAGAAAGGACACCCCTCTC	861
D	b	1161	AAACAGAAAGGACACCCCTCTC	1181

RESULT 9

; Sequence 300, Application US/10287436A
; Publication No. US20050202421A1

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? APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
? TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
? TITLE OF INVENTION: RHEUMATOID ARTHRITIS
? FILE REFERENCE: 10872.514656
? CURRENT APPLICATION NUMBER: US/10/287,436A
? CURRENT FILING DATE: 2002-10-31
? PRIOR APPLICATION NUMBER: US 60/336,220
? PRIOR FILING DATE: 2001-10-31
? NUMBER OF SEQ ID NOS: 1446
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 300
? LENGTH: 4839
? TYPE: DNA
? ORGANISM: Homo sapiens
US-10-287-436A-300

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Query Match	100.0%;	Score 861;	DB 9;	Length 4839;
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Best Local Similarity 100.0%; Pred. No. 1.9e-219;
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGACCCCTTGTATGGGGTCAACAGACCCCGCCGCGCCGCGGAGCCCATGTC 60
DB 321 ATGACCCCTTGTATGGGGTCAACAGACCCCGCCGCGCGCCGCGGAGCCCATGTC 380
QY 61 TCTGACGTGCACTGCAAAAGCTCTTTTGTCCAGAGATGAGATCAAGAGTGGAG 120
DB 381 TCTGACGTGCACTGCAAAAGCTCTTTTGTCCAGAGATGAGATCAAGAGTGGAG 440
QY 121 TTTTGTGATCATCATCATGCTGCTGATGATGATGATGATGATGATGATGATGAT 180
DB 441 TTTTGTGATCATCATCATGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 500
QY 181 CTGCTGACCACTAACAAGCTGCTGACAGCTCTTCACTAGCCGACAGCCAGGAGG 240
DB 501 CTGCTGACCACTAACAAGCTGCTGACAGCTCTTCACTAGCCGACAGCCAGGAGG 560
QY 241 AGGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 561 AGGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 620
QY 301 GCGACAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 621 GCGACAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 680
QY 361 GTGCGCCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 681 GTGCGCCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 740
QY 421 CAGCAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 741 CAGCAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 800
QY 481 TACGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 801 TACGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 860
QY 541 GAGTGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 861 GAGTGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 920
QY 601 AGGCTGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 921 AGGCTGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 980
QY 661 AGGCTGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 981 AGGCTGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1040
QY 721 GGGTCTCTCTTCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 780
DB 1041 GGGTCTCTCTTCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1100
QY 781 CTGCAACACACACACACACACACACACACACACACACACACACACACACACAC 840
DB 1101 CTGCAACACACACACACACACACACACACACACACACACACACACACACACAC 1160
QY 841 AAACAGAAAGACACCTCTC 861
DB 1161 AAACAGAAAGACACCTCTC 1181
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RESULT 10
US-09-796-753-55
Sequence 55, Application US/09796753
Publication No. US20030027998A1
GENERAL INFORMATION:
APPLICANT: McCarthy, Sean A.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-227-999
CURRENT APPLICATION NUMBER: US/09/796, 753

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QY 102 GAGATCAACGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 161
DB 2 GAGATCAACGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 61
QY 162 GGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 221
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CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/183,175
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 09/223,094
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/224,246
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/259,388
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/122,458
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: 09/312,359
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/336,536
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 09/342,687
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 09/345,464
PRIOR FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: 09/365,164
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 09/399,723
PRIOR FILING DATE: 1999-09-20
PRIOR APPLICATION NUMBER: 09/409,634
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 09/471,179
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 09/474,071
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/474,072
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/514,010
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: 09/516,745
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/572,002
PRIOR FILING DATE: 2000-05-14
PRIOR APPLICATION NUMBER: 09/597,993
PRIOR FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: 09/599,596
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 09/630,334
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: 09/606,565
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/606,317
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/665,666
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: 09/677,751
PRIOR FILING DATE: 2000-09-30
NUMBER OF SEQ ID NOS: 162
SEQ ID NO 55
LENGTH: 969
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (6)...(761)
US-09-796-753-55

Query Match 87.7%; Score 755.2; DB 3; Length 969;
Best Local Similarity 99.6%; Pred. No. 2.5e-191;
Matches 757; Conservative 0; Mismatches 3; Indels 0; Gaps 0;


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Db 62 GGTGTGTATATCACTGTCCTGAGGCACTAACAAGCTGTCTGACGGTCTTCATCAG 121
Qy 222 CCGGCAACCCAGGGGCGGAGGAGAGAAATGCTCTGTCTCAAGAAATGCTGTGGCC 281
Db 122 CCGGCAACCCAGGGGCGGAGGAGAGAAATGCTCTGTCTCAAGAAATGCTGTGGCC 181
Qy 282 CTGGAGAGGACAGTGTGAGGCAACGAAATCCAGAGCGGAGGCTTACCGCCCGCTCG 341
Db 182 CTGGAGAGGACAGTGTGAGGCAACGAAATCCAGAGCGGAGGCTTACCGCCCGCTCG 241
Qy 342 GCCCAGGAGCCGCTGCGCGTGCCTTCGCGCCGAGGAGCGCTTCAACGCTTCA 401
Db 242 GCCCAGGAGCCGCTGCGCGTGCCTTCGCGCCGAGGAGCGCTTCAACGCTTCA 301
Qy 402 GCCCAGGAGCCGCTGCGCGTGCCTTCGCGCCGAGGAGCGCTTCAACGCTTCA 461
Db 302 GCCCAGGAGCCGCTGCGCGTGCCTTCGCGCCGAGGAGCGCTTCAACGCTTCA 361
Qy 462 CGGGAGGAGGCGCCCACTCAAGGCGCCCTGCAACCTTCAGGTTGGGAGCCCGAGCA 521
Db 362 CGGGAGGAGGCGCCCACTCAAGGCGCCCTGCAACCTTCAGGTTGGGAGCCCGAGCA 421
Qy 522 GCACCTGGAATGAAACCGGAGTGTGTGCGGCAACCCCAAAAGAAACATCTTCAAG 581
Db 422 GCACCTGGAATGAAACCGGAGTGTGTGCGGCAACCCCAAAAGAAACATCTTCAAG 481
Qy 582 TGACCTGATGATGTGTGCGGAGTGTGTGCGGCGCCCTGCGCGGAGTGTGTGCGG 641
Db 482 TGACCTGATGATGTGTGCGGAGTGTGTGCGGCGCCCTGCGCGGAGTGTGTGCGG 541
Qy 642 CAGGCGGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 701
Db 542 CAGGCGGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 601
Qy 702 GGTATCGGCACTAACCGGAGTCTCTTCACAGCAGAGCAGTGTGTGTGTGTGTGTGT 761
Db 602 GGTATCGGCACTAACCGGAGTCTCTTCACAGCAGAGCAGTGTGTGTGTGTGTGTGT 661
Qy 762 CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 821
Db 662 CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 721
Qy 822 CTGGAGCAAGAGAGATTAACAGAAAGACACCTCTCTC 861
Db 722 CTGGAGCAAGAGAGATTAACAGAAAGACACCTCTCTC 761

RESULT 11
US-10-205-823-412
; Sequence 412, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gordatcheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Momsey, Angela M.
; APPLICANT: Glatc, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Duclun
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
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; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 412
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-412

Query Match 87.6%; Score 754.2; DB 5; Length 1141;
Best Local Similarity 98.3%; Pred. No. 4; de-191;
Matches 762; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 87 TTTGTTCAGAGCATGAGATCAAGAGCTGAGATTGTTCAAGTCATCATCTGTGT 146
Db 77 TCTCTCGGAAACAGGCAATGGCGAGCTGAGATTGTTCAAGTCATCATCTGTGT 136
Qy 147 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 206
Db 137 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 196
Qy 207 ACGGTCTTATATGACCGGAGCAGCGGAGGCGGAGGAGGAGGAGGAGGAGGAGG 266
Db 197 ACGGTCTTATATGACCGGAGCAGCGGAGGCGGAGGAGGAGGAGGAGGAGGAGG 256
Qy 267 AGATGCTGTGCGCTCGGAGAGCAGTGTGAGCAGCAAGAAATCCAGAGCGCAGGT 326
Db 257 AGATGCTGTGCGCTCGGAGAGCAGTGTGAGCAGCAAGAAATCCAGAGCGCAGGT 316
Qy 327 CTACGCGCGCTCGGCGCAACCGAGCGCTGCGCGCTGCGCGCTGCGCGCGGAGCG 386
Db 317 CTACGCGCGCTCGGCGCAACCGAGCGCTGCGCGCTGCGCGCTGCGCGCGGAGCG 376
Qy 387 CTTCACCGCTTCCAGGCGCACTATCGTACTGAGCAGAGATGAGATGAGATGAGAT 446
Db 377 CTTCACCGCTTCCAGGCGCACTATCGTACTGAGCAGAGATGAGATGAGATGAGAT 436
Qy 447 CATCTGCTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 506
Db 437 CATCTGCTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 496
Qy 507 TCGGAGCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 566
Db 497 TCGGAGCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 556
Qy 567 AACCATCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 626
Db 557 AACCATCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 616
Qy 627 CAGTAACTCGGAGCATGAGCGGCACTGCTACGAGGCGGCGGAGGAGGAGGAGGAGG 686
Db 617 CAGTAACTCGGAGCATGAGCGGCACTGCTACGAGGCGGCGGAGGAGGAGGAGGAGG 676
Qy 687 GCCCAGCTACAGGAGGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 746
Db 677 GCCCAGCTACAGGAGGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 736
Qy 747 CAGTGGGCGGCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 806
Db 737 CAGTGGGCGGCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 796
Qy 807 AGAGGCGGAGCATCTGAGCAAGAGAGATTAACAGAAAGACACCTCTC 861
Db 797 AGAGGCGGAGCATCTGAGCAAGAGAGATTAACAGAAAGACACCTCTC 851

RESULT 12
US-10-301-822-208
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 28, 2006, 09:50:15 ; Search time 6670 Seconds
(without alignments)
11257.901 Million cell updates/sec

Title: US-09-934-249-1

Perfect score: 1321
Sequence: 1 cgaccgcggtctcgagcga.....ctgcgtagtcgaaagcag 1321

Scoring table: OLIGO-NUC
Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word-size: 23

Total number of hits satisfying chosen parameters: 8868

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

Database :

GenEmb1:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_hlg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1321	100.0	1321	6	AX392417 Sequence
2	1302	98.6	4930	6	CS130796 Sequence
3	1229	93.0	4839	6	CO812357 Sequence
4	1229	93.0	4839	6	CO896247 Sequence
5	1229	93.0	4839	6	CO976475 Sequence
6	1229	93.0	4839	6	CO981430 Sequence
7	1229	93.0	4839	6	AF305616 Homo sapi
8	1178	89.2	1383	6	AX775889 Sequence
9	909	68.8	4519	6	CO894692 Sequence
10	861	65.2	861	6	AX392419 Sequence
11	838	63.4	1061	8	BC015918 Homo sapi
12	800	60.6	1140	6	AR336830 Sequence
13	800	60.6	1141	8	AF224278 Homo sapi
14	800	60.6	1818	8	AY128643 Homo sapi
15	800	60.6	4531	6	CS130842 Sequence
16	800	60.6	4538	6	CS130841 Sequence
17	785	57.2	785	6	AR336831 Sequence
18	749	56.7	969	6	BD272494 Secreted

19	749	56.7	1085	6	AX775887 Sequence
20	749	56.7	1913	6	BD272544 Secreted
21	744	56.3	969	6	BD272514 Secreted
22	704	53.3	759	6	BD272545 Secreted
23	701	53.1	753	6	BD272534 Secreted
24	701	53.1	756	6	BD272495 Secreted
25	698	52.8	969	6	BD272516 Secreted
26	698	52.8	969	6	BD272515 Secreted
27	647	49.0	1060	8	BC080635 Homo sapi
28	600	45.4	600	6	CO728942 Sequence
29	593	44.9	61505	8	AF305426 Homo sapi
30	593	44.9	130435	8	HS71807 Human DNA
31	560	42.4	1583	6	AX593655 Sequence
32	521	39.4	150224	8	HSU105917 Human DNA
33	401	30.4	408	6	AX071267 Sequence
34	302	22.9	693	6	AX392430 Sequence
35	271	20.5	812	6	BD226320 Pancreati
36	271	20.5	812	6	AX011709 Sequence
37	209	15.8	310	6	CO976479 Sequence
38	209	15.8	529	6	CO976481 Sequence
39	209	15.8	579	6	CO976478 Sequence
40	152	11.5	301	6	CO976480 Sequence
41	110	8.3	270	6	CO735730 Sequence
42	60	4.5	60	6	CO543985 Sequence
43	54	4.1	158243	14	CR956367 Sus scrof
44	52	3.9	183457	14	CR956387 Sus scrof
45	51	3.9	51	6	AX198565 Sequence
46	44	3.3	411	6	BD272547 Secreted
47	44	3.3	484	6	BD272546 Secreted
48	44	3.3	648	6	BD272535 Secreted
49	44	3.3	651	6	BD272505 Secreted
50	44	3.3	651	9	AF220208 Mus muscu
51	44	3.3	878	6	AX392428 Sequence
52	44	3.3	878	6	BC092094 Mus muscu
53	44	3.3	895	9	BC069890 Mus muscu
54	44	3.3	1079	9	BC023092 Mus muscu
55	44	3.3	1265	5	AJ720618 Gallus ga
56	44	3.3	1379	9	BC036995 Mus muscu
57	44	3.3	1713	6	BD272504 Secreted
58	44	3.3	1713	6	BD272517 Secreted
59	44	3.3	1713	6	BD272518 Secreted
60	44	3.3	1713	6	BD272519 Secreted
61	44	3.3	156698	9	AL837509 Mouse DNA
62	44	3.3	175847	14	AC110189 Mus muscu
63	44	3.3	231930	14	AC134911 Mus muscu
64	42	3.2	673	6	AX525744 Sequence
65	42	3.2	249554	14	AC139417 Ratius no
66	42	3.2	258632	14	AC111878 Ratius no
67	41	3.1	475	6	AX392431 Sequence
68	41	3.1	128625	9	AL837520 Mouse DNA
69	37	2.8	179741	14	AC116815 Mus muscu
70	34	2.6	640	6	AR617254 Sequence
71	34	2.6	2000	6	AX655988 Sequence
72	34	2.6	3046	8	HS4J757 AB065453 Homo sapi
73	34	2.6	44312	8	AB065453 Homo sapi
74	34	2.6	110000	14	AC106698 Ratius no
75	34	2.6	110000	14	CT005267_06 Continuation (7 of
76	34	2.6	110000	14	CT005267_07 Continuation (106
77	34	2.6	110000	15	AP008205_105 Continuation (223
78	34	2.6	110000	15	AP008210_222 Continuation (404
79	34	2.6	118883	8	AC009404 Homo sapi
80	34	2.6	118959	15	OSJNO0235 AL713593 Oryza sat
81	34	2.6	153308	15	AC118668 Genomic s
82	34	2.6	187409	9	AC151572 Mus muscu
83	34	2.6	198689	14	AC126463 Ratius no
84	34	2.6	219471	14	AC134632 Ratius no
85	34	2.6	221100	14	AC112841 Ratius no
86	34	2.6	233939	14	AC105853 Ratius no
87	34	2.6	237026	14	AC103439 Ratius no
88	34	2.6	237151	14	AC137424 Ratius no
89	34	2.6	242493	14	AC137322 Ratius no
90	34	2.6	247356	14	AC111257 Ratius no
91	34	2.6	266344	8	AC005158 Homo sapi

92	34	2.6	275229	14	AC098198	AC098198 Rattus no	c 165	32	2.4	258545	14	AC135666	AC135666 Rattus no
93	34	2.6	305075	14	AC106355	AC106355 Rattus no	c 166	32	2.4	259335	14	AC126194	AC126194 Rattus no
C 94	33	2.5	86146	14	AC023805	AC023805 Mus muscu	c 167	32	2.4	279534	14	AC114035	AC114035 Rattus no
C 95	33	2.5	101396	8	AC131182	AC131182 Homo sapi	c 168	32	2.4	281747	14	AC094865	AC094865 Rattus no
C 96	33	2.5	165212	9	AL596125	AL596125 Mouse DNA	c 169	32	2.4	296417	14	AC112730	AC112730 Rattus no
C 97	33	2.5	172172	14	AC069030	AC069030 Homo sapi	c 170	32	2.4	303425	14	AC111410	AC111410 Rattus no
98	33	2.5	229482	14	AC074149	AC074149 Mus muscu	c 171	31	2.3	359	6	AR617715	AR617715 Sequence
99	32	2.4	274	10	BV102379	BV102379 RPRMSE00	c 172	31	2.3	357	10	BV105358	BV105358 MARC 5563
100	32	2.4	577	6	CQ057943	CQ057943 Sequence	c 173	31	2.3	533	6	AR617857	AR617857 Sequence
101	32	2.4	577	6	CQ077251	CQ077251 Sequence	c 174	31	2.3	645	6	CQ609324	CQ609324 Sequence
102	32	2.4	577	6	CQ108252	CQ108252 Sequence	c 175	31	2.3	834	15	AK105087	AK105087 Oryza sat
103	32	2.4	577	6	CQ146881	CQ146881 Sequence	c 176	31	2.3	915	15	AK120273	AK120273 Oryza sat
104	32	2.4	577	6	CQ182292	CQ182292 Sequence	c 177	31	2.3	936	15	AK072488	AK072488 Oryza sat
105	32	2.4	577	6	CQ206688	CQ206688 Sequence	c 178	31	2.3	2332	6	AX747175	AX747175 Sequence
106	32	2.4	577	6	CQ230106	CQ230106 Sequence	c 179	31	2.3	2332	6	AK091771	AK091771 Homo sapi
107	32	2.4	577	6	CQ268254	CQ268254 Sequence	c 180	31	2.3	2808	6	CQ609323	CQ609323 Sequence
108	32	2.4	577	6	CQ305288	CQ305288 Sequence	c 181	31	2.3	28202	14	AC017459	AC017459 Drosophill
109	32	2.4	577	6	CQ342489	CQ342489 Sequence	c 182	31	2.3	59078	8	AL606807	AL606807 Human DNA
110	32	2.4	834	15	AK062882	AK062882 Oryza sat	c 183	31	2.3	67987	9	AL672157	AL672157 Mouse DNA
111	32	2.4	1804	9	BC026781	BC026781 Mus muscu	c 184	31	2.3	70811	14	AC117542	AC117542 Mus muscu
112	32	2.4	1810	9	BC058223	BC058223 Mus muscu	c 185	31	2.3	100580	8	BS000235	BS000235 Pan trogl
113	32	2.4	1964	6	CQ052940	CQ052940 Sequence	c 186	31	2.3	110000	15	BS000235	BS000235 Pan trogl
114	32	2.4	1964	6	CQ068034	CQ068034 Sequence	c 187	31	2.3	110000	15	AP008215_043	AP008215_043 Continuation (26 o
115	32	2.4	1964	6	CQ095094	CQ095094 Sequence	c 188	31	2.3	110000	15	AP008207_025	AP008207_025 Continuation (295
116	32	2.4	1964	6	CQ133842	CQ133842 Sequence	c 189	31	2.3	110000	15	AP008213_294	AP008213_294 Continuation (1295
117	32	2.4	1964	6	CQ172380	CQ172380 Sequence	c 190	31	2.3	114288	8	AP000590	AP000590 Homo sapi
118	32	2.4	1964	6	CQ201552	CQ201552 Sequence	c 191	31	2.3	115150	14	AP005736	AP005736 Oryza sat
119	32	2.4	1964	6	CQ217078	CQ217078 Sequence	c 192	31	2.3	134793	15	AP006441	AP006441 Oryza sat
120	32	2.4	1964	6	CQ256566	CQ256566 Sequence	c 193	31	2.3	147274	14	AP005588	AP005588 Oryza sat
121	32	2.4	1964	6	CQ292752	CQ292752 Sequence	c 194	31	2.3	149773	14	AC118209	AC118209 Mus muscu
122	32	2.4	1964	6	CQ229738	CQ229738 Sequence	c 195	31	2.3	151263	15	AP004333	AP004333 Oryza sat
C 123	32	2.4	2000	6	AK56401	AK56401 Sequence	c 196	31	2.3	157112	15	AP002872	AP002872 Oryza sat
C 124	32	2.4	2717	9	AB045590	AB045590 Rattus no	c 197	31	2.3	159524	8	AC155302	AC155302 Mus muscu
C 125	32	2.4	2825	15	AK120262	AK120262 Oryza sat	c 198	31	2.3	160456	9	BS000236	BS000236 Pan trogl
C 126	32	2.4	2916	13	CHKCMOPLP	CHKCMOPLP Chicken MRN	c 199	31	2.3	167029	15	AP002540	AP002540 Oryza sat
C 127	32	2.4	3171	13	AAFWMAF	AAFWMAF Avian muscu	c 200	31	2.3	170510	15	AP005589	AP005589 Oryza sat
C 128	32	2.4	3960	5	CHKCMFP	D25596 Gallus gall	c 201	31	2.3	174375	14	AC128360	AC128360 Rattus no
C 129	32	2.4	56475	8	AL353658	AL353658 Human DNA	c 202	31	2.3	174520	14	BS000234	BS000234 Pan trogl
C 130	32	2.4	73803	15	NCB11B22	AL356834 Neurospor	c 203	31	2.3	174520	14	AC157456	AC157456 Oryctolag
C 131	32	2.4	95637	15	BX842594	BX842594 Neurospor	c 204	31	2.3	180048	14	AC157456	AC157456 Oryctolag
C 132	32	2.4	110000	14	AC109084_1	Continuation (2 of	c 205	31	2.3	181751	14	AC160121	AC160121 Mus muscu
C 133	32	2.4	110000	15	AP008214_233	Continuation (234	c 206	31	2.3	183301	14	AC092487	AC092487 Homo sapi
C 134	32	2.4	110000	15	AP008207_279	Continuation (280	c 207	31	2.3	188489	2	AC012098	AC012098 Drosophill
C 135	32	2.4	111388	8	AC016655	AC016655 Homo sapi	c 208	31	2.3	188489	14	AC146153	AC146153 Pan trogl
C 136	32	2.4	115487	14	AC027344	AC027344 Homo sapi	c 209	31	2.3	188766	2	AC010708	AC010708 Drosophill
C 137	32	2.4	124752	8	AC010419	AC010419 Homo sapi	c 210	31	2.3	189982	14	AC079023	AC079023 Mus muscu
C 138	32	2.4	142182	15	AP004399	AP004399 Oryza sat	c 211	31	2.3	194151	9	AC152976	AC152976 Mus muscu
C 139	32	2.4	153223	14	AC018548	AC018548 Homo sapi	c 212	31	2.3	210608	8	AC006028	AC006028 Homo sapi
C 140	32	2.4	159324	8	AC146165	AC146165 Pan trogl	c 213	31	2.3	224817	14	AC133836	AC133836 Rattus no
C 141	32	2.4	160945	14	AC149910	AC149910 Strongylo	c 214	31	2.3	232183	14	AC111840	AC111840 Rattus no
C 142	32	2.4	160956	14	AC013637	AC013637 Homo sapi	c 215	31	2.3	232368	14	AC146962	AC146962 Oryctolag
C 143	32	2.4	161462	14	AC136669	AC136669 Rattus no	c 216	31	2.3	242299	14	AC110445	AC110445 Rattus no
C 144	32	2.4	172525	8	AC008514	AC008514 Homo sapi	c 217	31	2.3	247269	9	AC120819	AC120819 Rattus no
C 145	32	2.4	173837	8	AC124681	AC124681 Mus muscu	c 218	31	2.3	257790	14	AC115767	AC115767 Mus muscu
C 146	32	2.4	179372	14	AC040922	AC040922 Homo sapi	c 219	31	2.3	261710	14	AC107431	AC107431 Rattus no
C 147	32	2.4	179978	9	AC134561	AC134561 Mus muscu	c 220	31	2.3	276741	14	AC096301	AC096301 Rattus no
C 148	32	2.4	184123	14	AC163215	AC163215 Mus muscu	c 221	31	2.3	297155	14	AC095921	AC095921 Rattus no
C 149	32	2.4	190025	14	AC140145	AC140145 Homo sapi	c 222	31	2.3	315109	2	AB003509	AB003509 Oryza sat
C 150	32	2.4	190149	14	AC122097	AC122097 Rattus no	c 223	31	2.3	1922	15	AK100086	AK100086 Drosophill
C 151	32	2.4	192183	14	AC134492	AC134492 Rattus no	c 224	30	2.3	2383	8	BC021906	BC021906 Homo sapi
C 152	32	2.4	194459	15	AP003335	AP003335 Oryza sat	c 225	30	2.3	35119	14	AC151605	AC151605 Emblianla
C 153	32	2.4	198582	8	AC005291	AC005291 Homo sapi	c 226	30	2.3	35713	8	AC105344	AC105344 Homo sapi
C 154	32	2.4	202301	9	AC157950	AC157950 Mus muscu	c 227	30	2.3	70881	8	BX284660	BX284660 Human DNA
C 155	32	2.4	202525	9	AC153962	AC153962 Mus muscu	c 228	30	2.3	79951	8	HSJ908M4	HSJ908M4 Human DNA
C 156	32	2.4	204257	9	AC138676	AC138676 Mus muscu	c 229	30	2.3	99497	4	HS2931L6	HS2931L6 Human DNA
C 157	32	2.4	215695	9	AC148095	AC148095 Mus muscu	c 230	30	2.3	100974	14	AC104715	AC104715 Oryza sat
C 158	32	2.4	221080	14	AC106160	AC106160 Rattus no	c 231	30	2.3	110000	14	AC091352_1	AC091352_1 Continuation (3 of
C 159	32	2.4	222814	9	AC134591	AC134591 Mus muscu	c 232	30	2.3	110000	14	AC091352_2	AC091352_2 Continuation (3 of
C 160	32	2.4	226791	14	AC094199	AC094199 Rattus no	c 233	30	2.3	110000	14	AC091371_05	AC091371_05 Continuation (6 of
C 161	32	2.4	239018	14	AC106202	AC106202 Rattus no	c 234	30	2.3	110000	14	AC091371_06	AC091371_06 Continuation (7 of
C 162	32	2.4	242543	14	AC096128	AC096128 Rattus no	c 235	30	2.3	110000	15	AP008214_041	AP008214_041 Continuation (42 o
C 163	32	2.4	247458	14	AC164607	AC164607 Mus muscu	c 236	30	2.3	110000	15	AP008209_270	AP008209_270 Continuation (271
C 164	32	2.4	249600	14	AC126988	AC126988 Rattus no	c 237	30	2.3	110000	15	AP008211_255	AP008211_255 Continuation (256

C 238	30	2.3	111882	15	AC087851	AC087851 Oryza sat	311	2.2	446	6	C0058092	C0058092 Sequence
C 239	30	2.3	120627	14	AC104714	AC104714 Oryza sat	312	2.2	446	6	C0077409	C0077409 Sequence
C 240	30	2.3	136989	9	AC116710	AC116710 Mus muscu	313	2.2	446	6	C0108423	C0108423 Sequence
C 241	30	2.3	142215	8	AC133065	AC133065 Homo sapi	314	2.2	446	6	C0147064	C0147064 Sequence
C 242	30	2.3	148205	15	AP005606	AP005606 Oryza sat	315	2.2	446	6	C0182449	C0182449 Sequence
C 243	30	2.3	161701	14	AC117110	AC117110 Rattus no	316	2.2	446	6	C0206851	C0206851 Sequence
C 244	30	2.3	166406	9	AC124005	AC124005 Mus muscu	317	2.2	446	6	C0230291	C0230291 Sequence
C 245	30	2.3	169073	15	AC132491	AC132491 Oryza sat	318	2.2	446	6	C0268426	C0268426 Sequence
C 246	30	2.3	169585	14	AC078821	AC078821 Homo sapi	319	2.2	446	6	C0305460	C0305460 Sequence
C 247	30	2.3	174776	14	AC163265	AC163265 Rhinolph	320	2.2	446	6	C0342654	C0342654 Sequence
C 248	30	2.3	178807	14	AC166597	AC166597 Nomauscu	321	2.2	614	10	BV379979	BV379979 Sequence
C 249	30	2.3	179394	8	AC010619	AC010619 Homo sapi	322	2.2	646	10	HSNCAD1X1	HSNCAD1X1 Sequence
C 250	30	2.3	180585	9	AC131828	AC131828 Rattus no	323	2.2	631	10	BV018795	BV018795 Sequence
C 251	30	2.3	184908	9	AC102278	AC102278 Mus muscu	324	2.2	748	6	C0412532	C0412532 Sequence
C 252	30	2.3	185723	9	AC115316	AC115316 Rattus no	325	2.2	913	2	C0412532	C0412532 Sequence
C 253	30	2.3	194013	9	AL591905	AL591905 Mouse DNA	326	2.2	1012	8	AY542994	AY542994 Sequence
C 254	30	2.3	209245	14	AC151894	AC151894 Actus nan	327	2.2	1094	9	AF075291	AF075291 Sequence
C 255	30	2.3	209844	8	AC011495	AC011495 Homo sapi	328	2.2	1128	6	BC006245	BC006245 Sequence
C 256	30	2.3	211094	14	AC133625	AC133625 Rattus no	329	2.2	1154	8	BC089377	BC089377 Sequence
C 257	30	2.3	214493	14	AC097047	AC097047 Rattus no	330	2.2	1546	6	CS008054	CS008054 Sequence
C 258	30	2.3	217342	14	AC119700	AC119700 Rattus no	331	2.2	1546	6	AX928527	AX928527 Sequence
C 259	30	2.3	220179	14	AC115232	AC115232 Rattus no	332	2.2	1546	6	AX928527	AX928527 Sequence
C 260	30	2.3	223642	14	AC108290	AC108290 Rattus no	333	2.2	1546	6	AX951780	AX951780 Sequence
C 261	30	2.3	225465	14	AC126882	AC126882 Rattus no	334	2.2	1546	6	AX960058	AX960058 Sequence
C 262	30	2.3	227369	14	AC114469	AC114469 Rattus no	335	2.2	1546	6	AF075292	AF075292 Sequence
C 263	30	2.3	228381	14	AC103262	AC103262 Rattus no	336	2.2	1656	6	AX659956	AX659956 Sequence
C 264	30	2.3	230077	14	AC099450	AC099450 Rattus no	337	2.2	1710	9	BC003901	BC003901 Sequence
C 265	30	2.3	232900	14	AC103264	AC103264 Rattus no	338	2.2	2138	8	AK096881	AK096881 Sequence
C 266	30	2.3	233976	14	AC118078	AC118078 Rattus no	339	2.2	2506	8	BC098440	BC098440 Sequence
C 267	30	2.3	234626	14	AC098669	AC098669 Rattus no	340	2.2	2608	6	AX658366	AX658366 Sequence
C 268	30	2.3	237078	14	AC110347	AC110347 Rattus no	341	2.2	2627	15	AK103005	AK103005 Sequence
C 269	30	2.3	237317	14	AC097420	AC097420 Rattus no	342	2.2	2654	15	AK106611	AK106611 Sequence
C 270	30	2.3	239600	9	AC139128	AC139128 Mus muscu	343	2.2	2853	8	HSNCAD	HSNCAD Sequence
C 271	30	2.3	239932	14	AC095276	AC095276 Rattus no	344	2.2	2913	9	AF109773	AF109773 Sequence
C 272	30	2.3	240336	14	AC094844	AC094844 Rattus no	345	2.2	2987	8	BC006190	BC006190 Sequence
C 273	30	2.3	240510	14	AC134371	AC134371 Rattus no	346	2.2	3266	6	C0413290	C0413290 Sequence
C 274	30	2.3	246875	14	AC130059	AC130059 Rattus no	347	2.2	3431	6	C0717870	C0717870 Sequence
C 275	30	2.3	247664	14	AC125774	AC125774 Rattus no	348	2.2	3444	8	AF028706	AF028706 Sequence
C 276	30	2.3	247766	14	AC119322	AC119322 Rattus no	349	2.2	3681	8	AF152658	AF152658 Sequence
C 277	30	2.3	248294	14	AC133969	AC133969 Rattus no	350	2.2	4033	8	BC036470	BC036470 Sequence
C 278	30	2.3	248367	14	AC094853	AC094853 Rattus no	351	2.2	4122	6	C0824160	C0824160 Sequence
C 279	30	2.3	251003	14	AC131000	AC131000 Rattus no	352	2.2	5370	6	C0581298	C0581298 Sequence
C 280	30	2.3	251790	14	AC099003	AC099003 Rattus no	353	2.2	5464	2	AY051657	AY051657 Sequence
C 281	30	2.3	254460	14	AC132183	AC132183 Rattus no	354	2.2	5552	2	DR0P1C21A	DR0P1C21A Sequence
C 282	30	2.3	254650	14	AC128790	AC128790 Rattus no	355	2.2	5719	9	AF327569	AF327569 Sequence
C 283	30	2.3	256398	14	AC130952	AC130952 Rattus no	356	2.2	5750	9	DR0P1C21B	DR0P1C21B Sequence
C 284	30	2.3	257028	14	AC112276	AC112276 Rattus no	357	2.2	37996	6	C0581297	C0581297 Sequence
C 285	30	2.3	263297	14	AC127631	AC127631 Rattus no	358	2.2	44868	14	AC017345	AC017345 Sequence
C 286	30	2.3	265566	14	AC123187	AC123187 Rattus no	359	2.2	67995	14	AC100485	AC100485 Sequence
C 287	30	2.3	269740	14	AC133056	AC133056 Rattus no	360	2.2	52622	14	AC100485	AC100485 Sequence
C 288	30	2.3	271437	14	AC132564	AC132564 Rattus no	361	2.2	80101	2	AC004115	AC004115 Sequence
C 289	30	2.3	274467	14	AC113707	AC113707 Rattus no	362	2.2	93342	8	AC087245	AC087245 Sequence
C 290	30	2.3	274766	14	AC135283	AC135283 Rattus no	363	2.2	109339	8	HS137115	HS137115 Sequence
C 291	30	2.3	284834	14	AC135433	AC135433 Rattus no	364	2.2	110000	15	AP008214	AP008214 Sequence
C 292	30	2.3	286789	14	AC133723	AC133723 Rattus no	365	2.2	110000	15	AP008215	AP008215 Sequence
C 293	30	2.3	287586	14	AC103294	AC103294 Rattus no	366	2.2	110000	15	AP008218	AP008218 Sequence
C 294	30	2.3	291270	14	AC111506	AC111506 Rattus no	367	2.2	110000	15	AP008218	AP008218 Sequence
C 295	30	2.3	293834	14	AC135528	AC135528 Rattus no	368	2.2	110000	15	AP008207	AP008207 Sequence
C 296	30	2.3	349528	14	AC096443	AC096443 Rattus no	369	2.2	110000	15	AP008207	AP008207 Sequence
C 297	29	2.2	227	15	AY023293	AY023293 Oryza sat	370	2.2	110000	15	AP008207	AP008207 Sequence
C 298	29	2.2	230	15	AY022724	AY022724 Oryza sat	371	2.2	110000	15	AP008209	AP008209 Sequence
C 299	29	2.2	233	15	AY022902	AY022902 Oryza sat	372	2.2	110000	15	AP008210	AP008210 Sequence
C 300	29	2.2	383	4	AY308814	AY308814 Canis fam	373	2.2	110000	15	AP008211	AP008211 Sequence
C 301	29	2.2	401	6	C0053092	C0053092 Sequence	374	2.2	110000	15	AP008212	AP008212 Sequence
C 302	29	2.2	401	6	C0068196	C0068196 Sequence	375	2.2	119107	14	AC147494	AC147494 Sequence
C 303	29	2.2	401	6	C0095270	C0095270 Sequence	376	2.2	119116	14	AC152131	AC152131 Sequence
C 304	29	2.2	401	6	C0134027	C0134027 Sequence	377	2.2	119631	8	AC008888	AC008888 Sequence
C 305	29	2.2	401	6	C0172540	C0172540 Sequence	378	2.2	130569	8	CNS08088	CNS08088 Sequence
C 306	29	2.2	401	6	C0201717	C0201717 Sequence	379	2.2	131691	8	AC096765	AC096765 Sequence
C 307	29	2.2	401	6	C0217267	C0217267 Sequence	380	2.2	137220	15	AC135598	AC135598 Sequence
C 308	29	2.2	401	6	C0255831	C0255831 Sequence	381	2.2	137492	15	CNS08088	CNS08088 Sequence
C 309	29	2.2	401	6	C0292927	C0292927 Sequence	382	2.2	140620	15	AP003415	AP003415 Sequence
C 310	29	2.2	401	6	C0329907	C0329907 Sequence	383	2.2	145456	8	AL513366	AL513366 Sequence

C 384	2.2	146728	15	AP005396
C 385	2.2	146954	15	AP004635
C 386	2.2	151721	15	AP003943
C 387	2.2	152075	14	CNS07EPL
C 388	2.2	152090	15	CNS08C82
C 389	2.2	152406	14	AP005711
C 390	2.2	153388	15	AP003289
C 391	2.2	154378	15	AP001383
C 392	2.2	157981	15	AP006170
C 393	2.2	160135	14	BX649519
C 394	2.2	160894	14	AC135433
C 395	2.2	161564	9	AL772409
C 396	2.2	163946	8	AC146411
C 397	2.2	163461	2	AC008371
C 398	2.2	166677	2	AC115482
C 399	2.2	166745	8	AC096718
C 400	2.2	175154	8	AC093246
C 401	2.2	178882	14	AC158270
C 402	2.2	180355	15	AP005504
C 403	2.2	180673	9	AC068627
C 404	2.2	188010	14	AC134264
C 405	2.2	188908	9	AC110034
C 406	2.2	191110	14	AC121413
C 407	2.2	197082	8	AC006249
C 408	2.2	197714	14	AC128967
C 409	2.2	200491	8	AC007249
C 410	2.2	201430	14	HS7706
C 411	2.2	202825	14	AC161926
C 412	2.2	204136	9	AL772271
C 413	2.2	204407	14	AC021446
C 414	2.2	208848	14	AC139608
C 415	2.2	211795	14	AC125690
C 416	2.2	217838	14	AC132673
C 417	2.2	217867	14	AC095149
C 418	2.2	220480	14	AC023973
C 419	2.2	221776	14	AC136253
C 420	2.2	227533	14	AC094895
C 421	2.2	227605	14	AC121445
C 422	2.2	231930	14	AC134911
C 423	2.2	234137	8	AC157525
C 424	2.2	236966	14	AC113710
C 425	2.2	236967	9	AC126408
C 426	2.2	239069	14	AC108289
C 427	2.2	239591	14	AC128432
C 428	2.2	239945	14	AC094050
C 429	2.2	242130	14	AC108556
C 430	2.2	242151	14	CR956424
C 431	2.2	245174	14	AC095157
C 432	2.2	245582	9	AC140073
C 433	2.2	248254	14	AC133448
C 434	2.2	250175	14	AC160494
C 435	2.2	250188	14	AC110100
C 436	2.2	250207	14	AC096136
C 437	2.2	251158	14	AC117023
C 438	2.2	252115	14	AC131854
C 439	2.2	257028	14	AC112276
C 440	2.2	259747	14	AL136447
C 441	2.2	260041	14	AC153186
C 442	2.2	260041	14	AC153186
C 443	2.2	269117	14	AC115400
C 444	2.2	269155	9	AC109138
C 445	2.2	271135	14	AC105492
C 446	2.2	306076	2	AE003589
C 447	2.1	216	8	HUMHUNTPEA
C 448	2.1	224	15	AY023274
C 449	2.1	305	8	HUMEMELA
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C 452	2.1	401	10	BV192862
C 453	2.1	401	10	BV195133
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457	2.1	570	15	AK11017
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460	2.1	680	10	BV070089
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474	2.1	1094	15	AY532778
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C 485	2.1	1729	15	AK060965
C 486	2.1	1834	15	AK121202
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C 488	2.1	1947	6	AX460940
489	2.1	2000	6	AX655032
490	2.1	2145	6	CS031993
491	2.1	2145	6	CS032490
492	2.1	2145	6	CS036157
493	2.1	2145	6	CS040945
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495	2.1	2145	6	CS045109
496	2.1	2145	8	AF055377
C 497	2.1	2286	6	AX460942
C 498	2.1	2345	15	AK102975
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RESULT 1	AX392417	1321 bp	DNA	linear	PAT 23-MAR-2002
LOCUS	AX392417				
DEFINITION	Sequence 1 from Patent WO0216416.				
ACCESSION	AX392417				
VERSION	AX392417.1	GI:19700732			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
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	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
	Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Lee, R.T., Landeschulz, K.T., Kennedy, S.P., Thompson, J.F. and				
TITLE	Tu, T.G.				
JOURNAL	Diagnosis and treatment of cardiovascular conditions				
FEATRES	Patent: WO 0216416-A 1 28-FEB-2002;				
SOURCE	THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; PFIZER INC. (US)				
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ORIGIN

Query Match 100.0%; Score 1321; DB 6; Length 1321;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 1 CGACCGCGGCTCGAGAGCAACCGATCTCTTGAGATTGAATGAGAGAGAGGCG 60
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 61 CGCGCGCGCGCGCGCGAGGCGCTCGCTGAGGAAAGCTAGCGGCAAGGCTCAACCC 120
 61 CGCGCGCGCGCGCGCGAGGCGCTCGCTGAGGAAAGCTAGCGGCAAGGCTCAACCC 120
 121 GCGCGGAGCGCGCGCGCGCTCGCTGAGGAAAGCTAGCGGCAAGGCTCAACCC 180
 121 GCGCGGAGCGCGCGCGCGCTCGCTGAGGAAAGCTAGCGGCAAGGCTCAACCC 180
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 361 CG 420
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RESULT 2
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 LOCUS CS130796
 DEFINITION Sequence 82 from Patent WO2005064009.
 ACCESSION CS130796
 VERSION CS130796.1 GI:71792866
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1
 AUTHORS O'Brien, T.F.
 TITLE Classification of cancer
 JOURNAL Patent: WO 2005064009-A 82 14-JUN-2005;
 Arco Applied Biotechnology APS (DK)
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 /note="transmembrane, prostate androgen induced RNA (7")

ORIGIN

Query Match 98.6%; Score 1302; DB 6; Length 4930;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 1 AAACCGATCTCTCTGAGCTTGAATGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
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 61 GCGCGCTGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120

140 CTGCCAGCCCATTTTCCGGAGCCCAACCCGCGGGGCACTGCGACGCCCCCGGGGGCTGCCGA 199
121 CTGCCAGCCCATTTTCCGGAGCCCAACCCGCGGGGCACTGCGACGCCCCCGGGGGCTGCCGA 180
200 GGGGAGGCGGGGGGGGGGCGAGCGAGCGGGTCCCGGCACTGAGCCCCCGGGCGCCCG 259
181 GGGGAGGCGGGGGGGGGGCGAGCGAGCGGGTCCCGGCACTGAGCCCCCGGGGGCGCCCG 240
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241 GGAACCTTGGCGGAGCCCGAGCCCGGGGCGCGCTTCCCGCGCGCGCGCTC 300
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380 CCG 439
361 CCG 420
440 ACCCG 499
421 ACCCG 480
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481 TTGCTTCCAG 540
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680 GGAT 739
661 GGAT 720
740 TACG 799
721 TACG 780
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1040 AGTAATCTGCGGAGATCAGCG 1099
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1100 CCCACCTACAGAGAGAGATCAGCG 1159
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1160 AGTGGGCG 1219
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Qy 1280 CCGGAGGCGGCG 1321
Db 1261 CCGGAGGCGGCG 1302
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LOCUS CQ812357
DEFINITION Sequence 109 from Patent WO2004038020.
ACCESSION CQ812357
VERSION CQ812357.1 GI:47601977
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1. Waltig, R., Pousetka, A., Mollenhauer, J. and Schendendorf, D.
Target genes for the diagnosis and treatment of cancer
Patent: WO 2004038020-A 109 06-MAY-2004;
Deutsches Krebsforschungszentrum Stiftung des oeffentlichen n Rechts
(DE)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GAAAGCTTACGCGGAGAGGCTCAGCCCGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60
Qy 153 TTTCGAGCGGACCGCGGCGGAG 212
Db 61 TTTCGAGCGGACCGCGGCGGAG 120
Qy 213 GGGCGAGCGGAGCGCGGATCCCGGCACTGAGCCCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 272
Db 121 GGGCGAGCGGAGCGCGGATCCCGGCACTGAGCCCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Qy 273 GACCGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCG 332
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Qy 333 CCGAGCTTCCCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCG 392
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Db 301 GCCCG 360
Qy 453 CCGCGCGGAGCGCGGAGCTTCTGCGAGCTGCAAGCTGCAAGCTGCTTTGTTTCCAGAGCA 512
Db 361 CCGCGCGGAGCGCGGAGCTTCTGCGAGCTGCAAGCTGCAAGCTGCTTTGTTTCCAGAGCA 420
Qy 513 TGGAGATCAGGAGCTGAGGTTTGTTCAGATCAATCATCTGAGTGTGATGATGATGATGATGATGAT 572
Db 421 TGGAGATCAGGAGCTGAGGTTTGTTCAGATCAATCATCTGAGTGTGATGATGATGATGATGATGAT 480
Qy 573 TGGTGTGTGTATACGCTGCTGAGAGCACTCAAGCTGTGACAGGCTCTTCAATCA 632

Db 481 TGGTGTGTGTATCATCGTCTGCTGAGACCACTAAGACTGTCTGACAGGCTCTTATCA 540
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 QY 753 GAGCCACAGCAGCCGCTGGCCGCTGCGCCCTTGCAGCGAGAGCGCTTCAAGCCGCTTC 812
 Db 661 GAGCCACAGCAGCCGCTGGCCGCTGCGCCCTTGCAGCGAGAGCGCTTCAAGCCGCTTC 720
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 Db 721 AGCCCACTATCTCGTACCTGACAGCAGAGATGACCTTGCACCTCAATCTTGTGTGAG 780
 QY 873 AGGGGAGAGAGCCCACTTACAGAGGCTCTGACCTTCCAGCTTTCAGGAGCCCGGAGC 932
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RESULT 4
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 LOCUS Sequence 71 from Patent WO2004076614.
 DEFINITION CO896247
 ACCESSION CO896247.1 GI:55468096
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Homo sapiens (human)
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE

1 Hinzmann, B., Dahl, E., Rosenthal, A., Specht, T., Schmitt, A.,
 Beckmann, G., Brumentendorf, T., Kimmernann, H., Roepcke, S., Hermann, K.,
 Kitzhong, L., Pillarsky, C. and Staub, E.

Human nucleic acid sequences obtained from prostatic carcinomas
 Patent: WO 2004076614-A 71 10-SEP-2004;

Hinzmann, Bernd (DB); Dahl, Edgar (DB); Rosenthal, Andre (DB);
 Specht, Thomas (DB); Schmitt, Armin (DB)

FEATURES
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Query Match 93.0%; Score 1229; DB 6; Length 4839;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 633 GCGGCAACAGCGAGGGGCGAGAGAGAAAGATGCTTGTCTCAAGAGATGCTGTGGC 692
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 QY 993 GTGACCTGATGATAGTGCAGAGCTGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1052
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DB 1201 GGGCTGGGCTGCGTAGGTGAAAAGGAG 1229

RESULT 5
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LOCUS CQ976475 Sequence 166 from Patent WO2004113571.
ACCESSION CQ976475
VERSION CQ976475.1 GI:57975803
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
1
AUTHORS Einstein, R., McGowan, K.M. and Pando, M.P.
TITLE Prostate specific genes and the use thereof as targets for prostate
cancer therapy and diagnosis
JOURNAL Patent: WO 2004113571-A 166-29-DEC-2004;
Exonhit Therapeutics S.A. (FR)
FEATURES
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 GGAAGCTAGCGGCAAGGCTCAGCCCGGCGGCGGCGCGCCGCTGCGAGCCATT 152
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| | | | |
DB 61 TTCGCGAGCGGCAAGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
QY 213 GGGCGCAGCGAGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 272
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DB 121 GGGCGCAGCGAGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
QY 273 GACCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 332
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DB 181 GACCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
QY 333 CCGACCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 392
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DB 241 CCGACCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
QY 393 GCGCGCGCGCGCGCGCGCTCATGCAAGCTTATGAGGAGTCAAGAGCAAGCGCGCGCGG 452
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DB 301 GCGCGCGCGCGCGCGCGCTCATGCAAGCTTATGAGGAGTCAAGAGCAAGCGCGCGCGG 360

QY 453 CCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 512
| | | | |
DB 361 CCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
QY 513 TGGAGATCAAGAGAGCTGAGAGTTTGTTCATCATCATCATCATCATCATCATCATCATCAT 572
| | | | |
DB 421 TGGAGATCAAGAGAGCTGAGAGTTTGTTCATCATCATCATCATCATCATCATCATCATCAT 480
QY 573 TGGTGTGTGTGTATCATGCTGCTGTGAGCCTTCAAGAGCTGTGTGTGTGTGTGTGTGTGT 632
| | | | |
DB 481 TGGTGTGTGTGTATCATGCTGCTGTGAGCCTTCAAGAGCTGTGTGTGTGTGTGTGTGTGT 540
QY 633 GCGCGCAGCGAGGCGGCGGAGAGAGAGATGCGCTGCTCAAGAGAGAGAGAGAGAGAGAG 692
| | | | |
DB 541 GCGCGCAGCGAGGCGGCGGAGAGAGAGATGCGCTGCTCAAGAGAGAGAGAGAGAGAGAG 600
QY 693 CTTGAGAGAGCAGAGTGTAGAGGCAACCGAAATCCAGAGCGGAGGTCTAGCGCGCGCTC 752
| | | | |
DB 601 CTTGAGAGAGCAGAGTGTAGAGGCAACCGAAATCCAGAGCGGAGGTCTAGCGCGCGCTC 660
QY 753 GGGCCACGAGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 812
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DB 661 GGGCCACGAGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
QY 813 AGCCCACTTATCCGCTACCTGAGCAGAGATGCACTGCAAGCAGCAGCAGCAGCAGCAGC 872
| | | | |
DB 721 AGCCCACTTATCCGCTACCTGAGCAGAGATGCACTGCAAGCAGCAGCAGCAGCAGCAGC 780
QY 873 AGCGGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 932
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DB 781 AGCGGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840
QY 933 AGCAGCTGGAAGTGAACCGGAGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 992
| | | | |
DB 841 AGCAGCTGGAAGTGAACCGGAGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 900
QY 993 GTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1052
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DB 901 GTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
QY 1053 TCAGCGCCACGTCGTACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1112
| | | | |
DB 961 TCAGCGCCACGTCGTACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1020
QY 1113 AGGTATATGCGGCACTACCGGCGGCTCTCTTCCAGCAGCAGAGAGAGAGAGAGAGAG 1172
| | | | |
DB 1021 AGGTATATGCGGCACTACCGGCGGCTCTCTTCCAGCAGCAGAGAGAGAGAGAGAGAG 1080
QY 1173 CTTGCTGAGAGGAGAGCGGCGCTCCAGCAGCAGCAGATGCGCGCTTAAAGAGCGGAGCA 1232
| | | | |
DB 1081 CTTGCTGAGAGGAGAGCGGCGCTCCAGCAGCAGCAGATGCGCGCTTAAAGAGCGGAGCA 1140
QY 1233 TCTGAGCAAGAGAGAGATTAACAGAAAGACACCTCTTAAGGAGTCCGAGGAGGAGCG 1292
| | | | |
DB 1141 TCTGAGCAAGAGAGAGATTAACAGAAAGACACCTCTTAAGGAGTCCGAGGAGGAGCG 1200
QY 1293 GGGCTGGGCTGCGTAGGTGAAAAGGAG 1321
| | | | |
DB 1201 GGGCTGGGCTGCGTAGGTGAAAAGGAG 1229

RESULT 6
CQ981430 4839 bp DNA linear PAT 25-JAN-2005
LOCUS CQ981430 Sequence 285 from Patent EP1498424.
ACCESSION CQ981430
VERSION CQ981430.1 GI:58190720
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

KEKDKOKGHP.L"
polya_signal 2158..2163
polya_signal 2463..2468
polya_signal 4818..4823
ORIGIN

Query Match 93.0%; Score 1229; DB 8; Length 4839;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 93 GGAAGCTAGCGGAGAGGCTCAGCCCGCGGAGCGCGCGCCCGCTGCGACCCATT 152
DB 1 GGAAGCTAGCGGAGAGGCTCAGCCCGCGGAGCGCGCGCCCGCTGCGACCCATT 60
QY 153 TTCGGAGCGCACTCCGCGGCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 212
DB 61 TTCGGAGCGCACTCCGCGGCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
QY 213 GGGCGCAGCGGAGCGCGGCTCCGCGCACTGAGCCCGCGCGCGCGCGCGCGCGCG 272
DB 121 GGGCGCAGCGGAGCGCGGCTCCGCGCACTGAGCCCGCGCGCGCGCGCGCGCG 180
QY 273 GACCCGAGCCCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 332
DB 181 GACCCGAGCCCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
QY 333 CCGAGCTCCGCGGCG 392
DB 241 CCGAGCTCCGCGGCG 300
QY 393 GCG 452
DB 301 GCG 360
QY 453 CCG 512
DB 361 CCG 420
QY 513 TGGAGATCAGGAGCTGGAATTTGTCAGATCATATATGTTGTTGATGATGATG 572
DB 421 TGGAGATCAGGAGCTGGAATTTGTCAGATCATATATGTTGTTGATGATGATG 480
QY 573 TGGTGTGTGTATATCAGTGCCTGCGAGCGCACTAAGCTGTGCGAGCGCTTCATCA 632
DB 481 TGGTGTGTGTATATCAGTGCCTGCGAGCGCACTAAGCTGTGCGAGCGCTTCATCA 540
QY 633 GCGCGCAGCG 692
DB 541 GCGCGCAGCG 600
QY 693 CCGCGGAGAGCACTGTCAGGCAACGGAATCCCGAGCGCGCGCGCGCGCGCGCG 752
DB 601 CCGCGGAGAGCACTGTCAGGCAACGGAATCCCGAGCGCGCGCGCGCGCGCGCG 660
QY 753 GGGCGCAGCG 812
DB 661 GGGCGCAGCG 720
QY 813 AGCCCACTATCTGATCTGACAGCAAGATGCACTGCAACCACTTCGCTGTGAG 872
DB 721 AGCCCACTATCTGATCTGACAGCAAGATGCACTGCAACCACTTCGCTGTGAG 780
QY 873 ACGGGAGAGAGCG 932
DB 781 ACGGGAGAGAGCG 840
QY 933 AGCAGCTGGAATCTGAACCGGAGTGTGTGCGCGCAACCGCGCGCGCGCGCGCG 992
DB 841 AGCAGCTGGAATCTGAACCGGAGTGTGTGCGCGCAACCGCGCGCGCGCGCGCG 900
QY 993 GTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1052
DB 901 GTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960

QY 1053 TCAGCGCAGCTGCTACGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1112
DB 961 TCAGCGCAGCTGCTACGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1020
QY 1113 AGGTGATCGGCACTACCGCGGAGTCTCTTCGAGCAACGAGAGAGTGGCGCGCT 1172
DB 1021 AGGTGATCGGCACTACCGCGGAGTCTCTTCGAGCAACGAGAGAGTGGCGCGCT 1080
QY 1173 CTTTGTGAGGAGGAGCGCGCGCTCCACACACACATCGCGCGCGCGCGCGCGCG 1232
DB 1081 CTTTGTGAGGAGGAGCGCGCGCTCCACACACACATCGCGCGCGCGCGCGCGCG 1140
QY 1233 TCTGAGCAAGAGAGATTAACAGAAAGAGACCTCTCTAGAGTCCCGAGGAGCGCG 1292
DB 1141 TCTGAGCAAGAGAGATTAACAGAAAGAGACCTCTCTAGAGTCCCGAGGAGCGCG 1200
QY 1293 GGGCTGGGAGTGGTGTAGTGAAGAGCGAG 1321
DB 1201 GGGCTGGGAGTGGTGTAGTGAAGAGCGAG 1229

RESULT 8
AX775889 1383 bp mRNA linear PAT 14-JUN-2003
LOCUS
DEFINITION
Sequence 159 from Patent WO03048202.
ACCESSION
AX775889 GI:32693607
VERSION
AX775889.1 GI:32693607
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE
1 Matsuda, A. and Muramatsu, S.
NF-kB activating gene
Patent: WO 03048202-A 159 12-JUN-2003;
JOURNAL
Asahi Kasei Kabushiki Kaisha (JP)
FEATRES
Location/Qualifiers
source
1. 1383
/organism="Homo sapiens"
/mol_type="mRNA"
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321..1184
/note="unnamed protein product"

CDS

QY 93 GGAAGCTAGCGGAGAGGCTCAGCCCGCGGAGCGCGCGCGCGCGCGCGCGCGCG 152
DB 1 GGAAGCTAGCGGAGAGGCTCAGCCCGCGGAGCGCGCGCGCGCGCGCGCGCGCG 60
QY 153 TTCGGAGCGCACTCCGCGGCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 212
DB 61 TTCGGAGCGCACTCCGCGGCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
QY 213 GGGCGCAGCGGAGCGCGGCTCCGCGCACTGAGCCCGCGCGCGCGCGCGCGCGCG 272
DB 121 GGGCGCAGCGGAGCGCGGCTCCGCGCACTGAGCCCGCGCGCGCGCGCGCGCG 180

ORIGIN

Query Match 89.2%; Score 1178; DB 6; Length 1383;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db	601	AGCGTGGGGGGGCCCCCTGCGCCCCCAGCAGTAACTCGGGGCATCAGCGCCACGTGCTAGGAC	660
QY	1073	AGCGGCGGGCGCGATGGAGGGGCGCGCGCCACCTAGACGAGGTCTATGGCCACTACCCG	1132
Db	661	AGCGGCGGGCGCGATGGAGGGGCGCGCGCCACCTAGACGAGGTCTATGGCCACTACCCG	720
QY	1133	GGGTCTCTCTTCCAGCAGCAGAGAGAGAGTGGGCGCGCTCTTGTCTGAGGGGACCCGG	1192
Db	721	GGGTCTCTCTTCCAGCAGCAGAGAGAGTGGGCGCGCTCTTGTCTGAGGGGACCCGG	780
QY	1193	CTCCACCCACACACATGCGCGCCCTTAAGAGCGGACATCTTGGAGCAAAAGAGAGGAT	1252
Db	781	CTCCACCCACACACATGCGCGCCCTTAAGAGCGGACATCTTGGAGCAAAAGAGAGGAT	840
QY	1253	AAACGAGAAGGACACCTCTCTAGGGGTCCCGAGGGGGCGCGGCTGGGGCTGCGTAGGTG	1312
Db	841	AAACGAGAAGGACACCTCTCTAGGGGTCCCGAGGGGGCGCGGCTGGGGCTGCGTAGGTG	900
QY	1313	AAAAGGCGAG 1321	
Db	901	AAAAGGCGAG 909	

RESULT 10				
AX392419	AX392419	861 bp	DNA	linear
LOCUS	Sequence 3 from Patent WO0216416.			
DEFINITION				
ACCESSION	AX392419			
VERSION	AX392419.1	GI:19700734		

SOURCE	ORGANISM
Homo sapiens (human)	Homo sapiens

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.

AUTHORS
Lee, R. T., Landschulz, K. T., Kennedy, S. P., Thompson, J. F. and Turi, T. G.

JOURNAL
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; PFIZER INC. (US)
Patent: WO 0216416-A 3 28-FEB-2002;
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; PFIZER INC. (US)

TELEPHONE	LOCATION/QUARTER	SOURCE
	1. .861	/organism="Homo sapiens"

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CDS
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ORIGIN

Query Match	65.2%;	Score 861;	DB 6;	Length 861;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 861;	Conservative	0;	Mismatches 0;	Indels 0;
			Gaps	0;
QY	413	ATGCACCGCTTATGAGGGGTCAACAGACCCGCCGCCGCCGCCGCCGCCGAGCCCAATGTC	472	
DB	1	ATGCACCGCTTATGAGGGGTCAACAGACCCGCCGCCGCCGCCGCCGAGCCCAATGTC	60	
QY	473	TCCTGCACGTGCAACTGCAACGCTTTTGTTCACAGCATGAGATCAAGAGCTGGAG	532	
DB	61	TCCTGCACGTGCAACGCTTTTGTTCACAGCATGAGATCAAGAGCTGGAG	120	
QY	533	TTTGTTCAGATCATCATCATCGTGTGTCGATGATGTCATGTCGTGTCATCAAGTCC	592	

[illegible]

RESULT 11					
BC015918	BC015918	1061 bp	mRNA	linear	PRI 01-APR-2004
LOCUS	Homo sapiens transmembrane, prostatic androgen induced RNA,				mRNA
DEFINITION	(cDNA Clone IMAGE:4559576), partial cds.				
ACCESSION	BC015918				
VERSION	BC015918.1	GI:16198474			

SOURCE	ORGANISM
Homo sapiens (human)	
Homo sapiens	

REFERENCE
1 (bases 1 to 1061)
AUTHORS
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., ...

Klausner, R.D., Collins, F.S., Wagner, L., Schmenem, C.M., Schurter, J.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhac, N.T., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Ditschenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J.S., Udell, T.B., Toskin, Y.K.I., Scarinci, P., Rana, S.S., Loquellano, N.A., Peters, G.J.,

Db 644 CGTGCTACGGCAGGCGGGGGCGCATGAGGGGGCGCGCCACCTAACAGAGGTCATCG 703
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Db 704 GCCACTACCGGGGGTCTCTCTTCCAGACACAGCAGAGCATGTGGCCCGCTCTTCTGTGG 763
Qy 1182 AGGGGACCGGGGCTCCACACACACACATCGGGCCCTTAGAGAGGGGCGCATCTGGAGCA 1241
Db 764 AGGGGACCGGGGCTCCACACACACACATCGGGCCCTTAGAGAGGGGCGCATCTGGAGCA 823
Qy 1242 AAGAGAGATTAACAGAAAGACACCTCTCTAGAGGTCCCGAGGGGGCCGGGCTGGGG 1301
Db 824 AAGAGAGATTAACAGAAAGACACCTCTCTAGAGGTCCCGAGGGGGCCGGGCTGGGG 883
Qy 1302 CTGCGTAGTGAAAAAGCAG 1321
Db 884 CTGCGTAGTGAAAAAGCAG 903

RESULT 15
CS130842 4531 bp DNA linear PAT 02-AUG-2005
LOCUS Sequence 128 from Patent WO2005064009.
DEFINITION CS130842
ACCESSION CS130842 GI:71792912
VERSION CS130842.1
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS O'Brien, T.F.
TITLE Classification of cancer
JOURNAL Patent: WO 2005064009-A 128 14-JUL-2005;
Aros Applied Biotechnology APS (DX)
FEATURES
source location/Qualifiers
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ORIGIN
Query Match 60.6%; Score 800; DB 6; Length 4531;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 800; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 522 CGGAGCTGGAGTTGTTGATCATCATCATCGTGTGTGATGATGTGTGTGTG 581
Db 104 CGGAGCTGGAGTTGTTGATCATCATCATCGTGTGTGATGATGTGTGTGTG 163
Qy 582 TGATCAGCTGCTGCTGAGCCTACAGCTGTCTGACGGTCTTTCATCAGCCGACCA 641
Db 164 TGATCAGCTGCTGCTGAGCCTACAGCTGTCTGACGGTCTTTCATCAGCCGACCA 223
Qy 642 GCCAGGGCGGAGAGAGAAATGCTCTGTCTTGAGAGATGCTGTGGCTTGGAGA 701
Db 224 GCCAGGGCGGAGAGAGAAATGCTCTGTCTTGAGAGATGCTGTGGCTTGGAGA 283
Qy 702 GCAAGTGTCAAGGCAACGGAATCCAGAGCCGAGAGTTAGCCCCCGCTGGCCCAAG 761
Db 284 GCAAGTGTCAAGGCAACGGAATCCAGAGCCGAGAGTTAGCCCCCGCTGGCCCAAG 343
Qy 762 ACCGCTGGCGGCTGCGCCCTTCCGAGCGGAGAGCTTCCACGCTTCCAGCCCACT 821
Db 344 ACCGCTGGCGGCTGCGCCCTTCCGAGCGGAGAGCTTCCACGCTTCCAGCCCACT 403
Qy 822 ATCCGTACTCTGACAGCAGATGCACTGTCCACCCACCATCTCGTGTCAAGCGGGAGG 881
Db 404 ATCCGTACTCTGACAGCAGATGCACTGTCCACCCACCATCTCGTGTCAAGCGGGAGG 463
Qy 882 AGCCCCACCTTACCAAGGGGCCCTGACCTTCAAGCTTGGGAGCCCGAGACAGAGCTGG 941

Db 464 AGCCCCACCTTACAGGGGCCCTTGACACCTTCAGCTTGGGAGCCCGAGACAGACTGG 523
Qy 942 AACTGAACCGGGAGTGTGTGCGGACACCCCAACAGAACATCTTTCAGAGTGAAGCTGA 1001
Db 524 AACTGAACCGGGAGTGTGTGCGGACACCCCAACAGAACATCTTTCAGAGTGAAGCTGA 583
Qy 1002 TGGATATGTGCAAGGTGTGGGGGGCCCTGCGCCCGCCAGAGTAACTGGGGCATGAGGCCA 1061
Db 584 TGGATATGTGCAAGGTGTGGGGGGCCCTGCGCCCGCCAGAGTAACTGGGGCATGAGGCCA 643
Qy 1062 CGTGCTACGCGCAGCGGGCGGCGATGAGAGGGGCGCGCCCACTTACAGGAGTATCG 1121
Db 644 CGTGCTACGCGCAGCGGGCGGCGATGAGAGGGGCGCGCCCACTTACAGGAGTATCG 703
Qy 1122 GCCACTACCGGGGGTCTCTCTTCCAGACACAGCAGAGCATGTGGCCCGCTCTTGTGG 1181
Db 704 GCCACTACCGGGGGTCTCTCTTCCAGACACAGCAGAGCATGTGGCCCGCTCTTGTGG 763
Qy 1182 AGGGGACCGGGGCTCCACACACACATCGGGCCCTTAGAGAGGGGCGCATCTGGAGCA 1241
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Qy 1242 AAGAGAGATTAACAGAAAGACACCTCTCTAGAGGTCCCGAGGGGGCCGGGCTGGGG 1301
Db 824 AAGAGAGATTAACAGAAAGACACCTCTCTAGAGGTCCCGAGGGGGCCGGGCTGGGG 883
Qy 1302 CTGCGTAGTGAAAAAGCAG 1321
Db 884 CTGCGTAGTGAAAAAGCAG 903

RESULT 16
CS130841 4538 bp DNA linear PAT 02-AUG-2005
LOCUS Sequence 127 from Patent WO2005064009.
DEFINITION CS130841
ACCESSION CS130841 GI:71792911
VERSION CS130841.1
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS O'Brien, T.F.
TITLE Classification of cancer
JOURNAL Patent: WO 2005064009-A 127 14-JUL-2005;
Aros Applied Biotechnology APS (DX)
FEATURES
source location/Qualifiers
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/note="transmembrane, prostate androgen induced RNA (T")

ORIGIN
Query Match 60.6%; Score 800; DB 6; Length 4538;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 800; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 522 CGGAGCTGGAGTTGTTGATCATCATCATCGTGTGTGATGATGTGTGTGTG 581
Db 111 CGGAGCTGGAGTTGTTGATCATCATCATCGTGTGTGATGATGTGTGTGTG 170
Qy 582 TGATCAGCTGCTGCTGAGCCTACAGCTGTCTGACGGTCTTTCATCAGCCGACCA 641
Db 171 TGATCAGCTGCTGCTGAGCCTACAGCTGTCTGACGGTCTTTCATCAGCCGACCA 230
Qy 642 GCCAGGGCGGAGAGAGAAATGCTCTGTCTTGAGAGATGCTGTGGCTTGGAGA 701
Db 231 GCCAGGGCGGAGAGAGAAATGCTCTGTCTTGAGAGATGCTGTGGCTTGGAGA 280

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Db	210	TGATCAGTGCCTGCTGTAGCCACTACAAAGCTGTCTGACGGTCTTCAATCAGCCGGACACA	269
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Db	270	GCCAGGGGCGGAGGAGAAAGATGCCCTGTCTTCAGAAAGATGCTGTGGCCCTTCGGAGA	329
QY	702	GCAAGTGTCAAGGCAAGGAAATCCCAAGGCGGAGCTTACACCGCTTCGAGCCCAACG	761
Db	330	GCAAGTGTCAAGGCAAGGAAATCCCAAGGCGGAGCTTACACCGCTTCGAGCCCAACG	389
QY	762	ACCGCTTGAGCGTGCCTCCGCTTCGAGGAGGAGCGCTTTCACACCGCTTCGAGCCCACT	821
Db	390	ACCGCTTGAGCGTGCCTCCGCTTCGAGGAGGAGCGCTTTCACACCGCTTCGAGCCCACT	449
QY	822	ATCCGTACTGAGCAGCAGATGCACTTGCCACCCACCATCTCGCTGTCAAGCGGGAGG	881
Db	450	ATCCGTACTGAGCAGCAGATGCACTTGCCACCCACCATCTCGCTGTCAAGCGGGAGG	509
QY	882	AGCCCCACCTTACCAAGGCGCCCTGCAACCTTCAGCTTCGGAGACCCGAGCAGAGCTGG	941
Db	510	AGCCCCACCTTACCAAGGCGCCCTGCAACCTTCAGCTTCGGAGACCCGAGCAGAGCTGG	569
QY	942	AAGTGAACCGGGAGTCCGCTGCGGCGCACCCCAACAGAAACCATCTTTCAGACGTGACCTGA	1001
Db	570	AAGTGAACCGGGAGTCCGCTGCGGCGCACCCCAACAGAAACCATCTTTCAGACGTGACCTGA	629
QY	1002	TGAGTAGTGCCAGGCTGGGCGGCGCCCTTGCGCCGCCAGCATGTAATCTCGGAGCATAGCGCCA	1061
Db	630	TGAGTAGTGCCAGGCTGGGCGGCGCCCTTGCGCCGCCAGCATGTAATCTCGGAGCATAGCGCCA	689
QY	1062	CGTGTCTAAGGAGAGGGGCGGCGGCGCATGGAAGGGGCGCGGCCCACTTACAGGAGGTCATCG	1121
Db	690	CGTGTCTAAGGAGAGGGGCGGCGGCGCATGGAAGGGGCGCGGCCCACTTACAGGAGGTCATCG	749
QY	1122	GCACTACCCGGGCGTCTCTTCCAGACACAGCAGACAGTGGGCGCGCTCTCTTGTCTGG	1181
Db	750	GCACTACCCGGGCGTCTCTTCCAGACACAGCAGACAGTGGGCGCGCTCTCTTGTCTGG	809
QY	1182	AGGGGAGCCGGGCTCCACCCACACACATCGCGCCCTTGAAGAGGCGAGCCCATCTGGAGACA	1241
Db	810	AGGGGAGCCGGGCTCCACCCACACACATCGCGCCCTTGAAGAGGCGAGCCCATCTGGAGACA	869
QY	1242	AAGAGAAAGATTAACAGAAAGGACACCTCTCTTGAAGGCGCCCAAGGGGGCGGGGCTGGGG	1301
Db	870	AAGAGAAAGATTAACAGAAAGGACACCTCTCTTGAAGGCGCCCAAGGGGGCGGGGCTGGGG	929
QY	1302	CTGGCTAGGTGAAAAAGGCGAG 1321	
Db	930	CTGGCTAGGTGAAAAAGGCGAG 949	

RESULT 21

BD272514

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

669 bp DNA linear PAT 17-JUL-2003

Secreted proteins and nucleic acids encoding chem.

BD272514

BD272514.1 GI:33082282

JP 2002539773-A/23.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (baaes 1 to 969)

Barnes,T.M., Holtzman,D.A., Sharp,J.D. and Fraser,C.C.

Secreted proteins and nucleic acids encoding chem

Patent: JP 2002539773-A 23 26-NOV-2002;

MILLENNIUM PHARMACEUTICALS INC

OS Homo sapiens (human)

PN JP 2002539773-A/23

PD 26-NOV-2002

PF 01-MAR-2000 JP 2000602247

PR 01-MAR-1999 US 60/122458

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[illegible]

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Db	182	GCAAGGTGTCAGGGAAGGAAATCC	CAGAGGCTTACGCCCCGCTCGGCCCAACG	241
Qy	762	ACCGCTTGCGCGTGC	CCGCTTCGCGAGGAGCGCTTCCACCGCTTCCAGGCCACT	821
Db	242	ACCGCTTGCGCGTGC	CCGCTTCGCGAGGAGCGCTTCCACCGCTTCCAGGCCACT	301
Qy	822	ATCCGTA	CTTGACGACGATGCACTTGCCACCCACATCTCGCTGTCAAGCGGGAGG	881
Db	302	ATCCGTA	CTTGACGACGATGCACTTGCCACCCACATCTCGCTGTCAAGCGGGAGG	361
Qy	882	AGCCCCACCTTACCAAGGCGCC	CTGACACCTCCAGCTTCGGAGACCCCGAGCAGAGCTGG	941
Db	362	AGCCCCACCTTACCAAGGCGCC	CTGACACCTCCAGCTTCGGAGACCCCGAGCAGAGCTGG	421
Qy	942	AACCTGAACCGGGAGT	CGGTGCGCGCACCCCCAAACAGAAACCATTTTGACAGTGA	1001
Db	422	AACCTGAACCGGGAGT	CGGTGCGCGCACCCCCAAACAGAAACCATTTTGACAGTGA	481
Qy	1002	TGATAGTGCAGGCTG	GGCGCGCCCTGCCCCCAGCAGTAACTCGGGCATCAGCGCCA	1061
Db	482	TGATAGTGCAGGCTG	GGCGCGCCCTGCCCCCAGCAGTAACTCGGGCATCAGCGCCA	541
Qy	1062	CGTCTAGAGGAGAGCGGCGGGG	CGATGGAAGGGCGCGGCCCACTTACAGAGGATCATG	1121
Db	542	CGTCTAGAGGAGAGCGGCGGGG	CGATGGAAGGGCGCGGCCCACTTACAGAGGATCATG	601
Qy	1122	GCACTACCCGGGGTCTCT	CTTCCAGACACAGAGAGAGTGGGCGGCTCTTGTCTGG	1181
Db	602	GCACTACCCGGGGTCTCT	CTTCCAGACACAGAGAGAGTGGGCGGCTCTTGTCTGG	661
Qy	1182	AGGGGAGCCCGGCTCC	ACCAACAACATCGCGCCCTTGAAGAGGCGAGCCCATTTGGAGCA	1241
Db	662	AGGGGAGCCCGGCTCC	ACCAACAACATCGCGCCCTTGAAGAGGCGAGCCCATTTGGAGCA	721
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DEFINITION	Secreted proteins and nucleic acids encoding them.			PAT 17-JUL-2003
ACCESSION	BD272495.1	GI:33082263		
VERSION	JP 2002539773-A/4.			
KEYWORDS	Homo sapiens (human)			
SOURCE	Homo sapiens			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.			
REFERENCE	1 (bases 1 to 756)			
AUTHORS	Barnes,T.M., Holtzman,D.A., Sharp,J.D. and Fraser,C.C.			
TITLE	Secreted proteins and nucleic acids encoding them			
JOURNAL	Patent: JP 2002539773-A 4 26-NOV-2002;			
COMMENT	MILLENNIUM PHARMACEUTICALS INC			
	OS Homo sapiens (human)			
	PN JP 2002539773-A/4			
	PD 26-NOV-2002			
	PF 01-MAR-2000 JP 2000602247			
	PI 01-MAR-1999 US 60/122458			
	PR THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CHRISTOPHER C FRASER			
	PC C12N15/09, C07K14/47, C07K16/18, C12N5/10, C12P21/02, C12Q1/68, PC G01N33/15,			

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Db	190	GCACAGTGTCAGGCAAGAAAGAAATCCAGAGCGCGAGAGCTTAAGCCCGCCTCTGGCCCAACG	249
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OY	1122	GCCACTAACCCGGGGTCTCTCTTCCAGACACACAGACAGACATGTGGGCGCTCTTGTCTGG	1181
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OY	1302	CTGGCTAGGTGTAATAAAGGACG 1321	
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LOCUS			
DEFINITION		Homo sapiens transmembrane, prostate androgen induced RNA, transcript variant 2, mRNA (CDNA clone MGC:99523 IMAGE:6569922), complete cds.	
ACCESSION		BC080635	
VERSION		BC080635.1 GI:51593770	
KEYWORDS		MGC.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo	
AUTHORS		1 (Daeas 1 to 1060)	
		Strausberg RU, Feilngold EA, Grouse LH, Derge JG, Klausner RD, Collins FS, Wagner L, Sherman CM, Schuler GD, Altschul SF, Zeeberg B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T, Max SI, Wang J, Heish F, Blatchenko L, Marinsina K, Farmer AD, Rudolph GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavini TL, Schaefer TE, Brownstein MJ, Uebin T, Toshiyuki S, Cavanini P, Prange C, Rana SS, Loquellano NA, Peters GJ, Abramson RD, Mollahy SJ, Bosak SA, McSwan PJ, McKernan KJ, Malek JA, Gunaratne PH, Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Huiyik SW, Villalon D, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J, Helton E, Kettman M, Madan A, Rodriguez S, Sanchez A, Whitting M, Madan A, Young AC, Shvchenko Y, Bouffard GG, Blakeley RW,	

TITLE Kites, such as nucleic acid arrays, comprising a majority of

humanexons or transcripts, for detecting expression and other uses

thereof Patent: WO 02068579-A 14876 06-SRP-2002;

JOURNAL PB Corporation (NY) (US)

JOURNAL up-regulated in renal cell carcinoma and other solid tumours
REFERENCE 2 (bases 1 to 61505)
AUTHORS Rae, F.K., Hooper, J.D., Nicol, D.L. and Clements, J.A.
TITLE Direct Submission
JOURNAL Submitted (13-SEP-2000) Centre for Molecular Biotechnology,
Queensland University of Technology, 2 George St, Brisbane, QLD
4001, Australia

FEATURES
SOURCE location/Qualifiers
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/db_xref="taxon:9606"

ORIGIN

Query Match 45.4%; Score 600; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 5.6e-287;
Matches 600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 737 GTCTAGCCGCCCTTCGAGAGACAGAGTCAAGCAATCCAGAGCCGAG 796
DB 61 GTCTAGCCGCCCTTCGAGAGACAGAGTCAAGCAATCCAGAGCCGAG 120
QY 797 CGCTTCACCGCTTCGAGAGACAGAGTCAAGCAATCCAGAGCCGAG 856
DB 121 CGCTTCACCGCTTCGAGAGACAGAGTCAAGCAATCCAGAGCCGAG 180
QY 857 ACCATCTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 916
DB 181 ACCATCTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
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DB 241 CTTCGGGACCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
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RESULT 29

AP305426 61505 bp DNA linear PRI 12-OCT-2001

LOCUS Homo sapiens solid tumor-associated 1 protein (STAG1/PMEP1) gene,

DEFINITION complete cds.

ACCESSION AF305426

VERSION AF305426.1 GI:15824468

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

FEATURES
SOURCE location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.7e-283;
Matches 593; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 57363 AGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 57422
QY 849 TGCCACCAACCATCTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 908
DB 57423 TGCCACCAACCATCTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 57482
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DB 57483 CCTTCACGCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 57542
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DB 57543 CCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 57602
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Qy 1269 CTCCTAGAGGTCCTCCAGGGGGCCGGGCTGGGCTGCTAGCTGAAAGGCG 1321
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RESULT 30
HS718U7/c
LOCUS
DEFINITION
Human DNA sequence from clone RP4-718U7 on chromosome 20q13.31-13.33 Contains the PCK1 gene for soluble phosphoenolpyruvate carboxykinase 1, the ZBP1 gene for 2-DNA binding protein 1, the 3' end of the TMEPA1 gene for transmembrane prostate androgen induced mRNA, two putative novel genes, the 5' end of the CTCFL gene for CCTC-binding factor (zinc finger)-like and a CpG island, complete sequence.

ACCESSION
VERSION
KEYWORDS
AL035541
AL035541.15 GI:11546043
HTG: C20orf183; CpG island; CTCFL; DLM-1; macrophage protein; PCK1; phosphoenolpyruvate carboxykinase; PWERP1; TMEPA1; transmembrane protein; ZBP1.

SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 130435)

REFERENCE
AUTHORS
JOURNAL
Sehra, H.
Direct Submission
Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk
Chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr20
RP4-718U7 is from the library RPCI-4 constructed by the group of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2

COMMENT
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: vegas@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
Location/Qualifiers
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QY 241 TGAAGCG 300
DB 52656 TGAAGCG 52597
QY 301 CTCCCG 360
DB 52596 CTCCCG 52537
QY 361 CCCCG 420
DB 52536 CCCCG 52477
QY 421 CTTCATGGGGGTCAACAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
DB 52476 CTTCATGGGGGTCAACAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCG 52417
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RESULT 33
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LOCUS AX071267
DEFINITION Sequence 1739 from Patent WO0102566.
ACCESSION AX071267
VERSION AX071267.1 GI:12581618
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE
AUTHORS
1 Williams, L.T., Escobedo, J., Imitis, M.A., Garcia, P.D., Klinger, J.,
Kassam, A., Reinhard, C., Randazzo, F., Kennedy, G.C., Pot, D.,
Lambson, G., Drmanac, R., Ckenjakov, R., Drmanac, S., Dickson, M.,
Labat, I., Leschowitz, D., Kita, D., Garcia, V. and Strache-Crain, B.
TITLE
JOURNML Human genes and gene expression products
Patent: WO 0102568-A 1739 11-JAN-2001;
CHIRON CORPORATION (US); HYSEQ, INC. (US)
FEATURES
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 6.5e-188;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 643 CCAGGGGCGAGAGAGAGATGCTGTCTCTGAGAGATGCTGTGAGAGAG 702
DB 68 CGAGGGGCGAGAGAGAGATGCTGTCTCTGAGAGATGCTGTGAGAGAG 127
QY 703 CACAGTGCAGCAAGCAAGATCCAGAGCGGAGGTCTACGCGCGCTCGGCCACCGA 762
DB 128 CACAGTGCAGCAAGCAAGATCCAGAGCGGAGGTCTACGCGCGCTCGGCCACCGA 187
QY 763 CCGCTGAGCGTGCCTCTGCGCCAGCGGAGACGCTTCAACGCTTCAGGCCACCTA 822
DB 188 CCGCTGAGCGTGCCTCTGCGCCAGCGGAGACGCTTCAACGCTTCAGGCCACCTA 247
QY 823 TCCGTAAGTGCAGCAAGATGCACTGCAACCAACCACTCTGCTGTCAGAGGGAGGA 882
DB 248 TCCGTAAGTGCAGCAAGATGCACTGCAACCAACCACTCTGCTGTCAGAGGGAGGA 307
QY 883 GCCCCACCTTACAGAGGCGCCCTGCAACCTTCAGCTTGGAGACCCGAGAGAGCTGGA 942
DB 308 GCCCCACCTTACAGAGGCGCCCTGCAACCTTCAGCTTGGAGACCCGAGAGAGCTGGA 367
QY 943 ACTGAACCGGAGATGCTGCGCGCAACCCCAAGAAACCA 983
DB 368 ACTGAACCGGAGATGCTGCGCGCAACCCCAAGAAACCA 408
RESULT 34
AX392430 693 bp DNA linear PAT 23-MAR-2002
LOCUS AX392430
DEFINITION Sequence 14 from Patent WO0216416.
ACCESSION AX392430
VERSION AX392430.1 GI:19700746
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS
1 Lee, R.T., Landschulz, K.T., Kennedy, S.P., Thompson, J.F. and
Turt, T.G.
TITLE
JOURNAL Diagnosis and treatment of cardiovascular conditions
Patent: WO 0216416-A 14 28-FEB-2002;
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US); PFIZER INC. (US)
FEATURES
source
1..693
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 22.9%; Score 302; DB 6; Length 693;
Best Local Similarity 100.0%; Pred. No. 1.2e-118;
Matches 302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 885 CCCACCCCTTACGAGGCGCCCTTGCACCTTCGAGCTTCGAGGAGCGAGCTGAGAC 944
DB 587 CCCACCCCTTACGAGGCGCCCTTGCACCTTCGAGCTTCGAGGAGCGAGCTGAGAC 528

QY 945 TGAACCGGAGTCGCTGCGCGCACCCCAACAGAACCATCTTCGACAGTGAAGCTGATG 1004
DB 527 TGAACCGGAGTCGCTGCGCGCACCCCAACAGAACCATCTTCGACAGTGAAGCTGATG 468

QY 1005 ATAGTGCAGAGCTGGGCGCGCCCTTCGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1064
DB 467 ATAGTGCAGAGCTGGGCGCGCCCTTCGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 408

QY 1065 GCTACGCGAGCGGCGCGCGCATGAGGAGCGCGCGCCACCTTACGAGGAGTGAAGTGAAGT 1124
DB 407 GCTACGCGAGCGGCGCGCGCATGAGGAGCGCGCGCCACCTTACGAGGAGTGAAGTGAAGT 348

QY 1125 ACTACCGCGGCTCTCTTCGACGACGACGAGAGTGGCGCGCTCTTCGAGAGTGAAGT 1184
DB 347 ACTACCGCGGCTCTCTTCGACGACGACGAGAGTGGCGCGCTCTTCGAGAGTGAAGT 288

QY 1185 GG 1186
DB 287 GG 286

RESULT 35
BD226320 812 bp DNA linear PAT 17-JUL-2003
LOCUS BD226320
DEFINITION Pancreatic cancer tissue-origin human nucleic acid sequence.
ACCESSION BD226320.1 GI:33036090
VERSION JP 2002512795-A/105
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
REFERENCE 1 (bases 1 to 812)
AUTHORS Specht,T., Hinzmann,B., Schmitt,A., Pilarsky,C., Dahl,E. and Rosenthal,A.
TITLE Pancreatic cancer tissue-origin human nucleic acid sequence
JOURNAL Patient: JP 2002512795-A/105 08-MAY-2002;
COMMENT METAGEN GSEBELSCHAFT FUER GENOM FORSCHUNG MBH
OS Homo sapiens (human)
PN JP 2002512795-A/105
PD 08-MAY-2002
PF 19-APR-1999 JP 2000546002
PR 28-APR-1998 DE 198 20 190.7
PI THOMAS SPECHT, BERND HINZMANN, ARMIN SCHMITT, CHRISTIAN PILARSKY,
PI EDGAR DAHL,
PI ANDRE ROSENTHAL
PC C12N15/09,A61K38/00,A61K48/00,A61P1/18,A61P35/00,C07K14/435,
PC C07K16/18,
PC C12N5/10,C12P21/02,C12P21/08,C12N15/00,A61K37/02,C12N5/00 CC
Pancreatic cancer tissue-origin human nucleic acid sequence FH
Key Location/Qualifiers
FT source 1..812
FT location/Qualifiers
1..812
/organism="Homo sapiens (human)"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

FEATURES
source 1..812
location/Qualifiers
1..812
/organism="Homo sapiens (human)"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 20.5%; Score 271; DB 6; Length 812;
Best Local Similarity 99.7%; Pred. No. 3.4e-123;
Matches 321; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 585 TCAGTGTCTGTGAGGCACTACAGCTGTCTGCAAGTCTTTCATCAAGCGGACAGCC 644
DB 426 TCAGTGTCTGTGAGGCACTACAGCTGTCTGCAAGTCTTTCATCAAGCGGACAGCC 485

QY 645 AGGGGCGGAGGAGGAGATGCTCTGCTCAGAAAGATGCTGTGAGCTCTCGGAGCA 704
DB 486 AGGGGCGGAGGAGGAGATGCTCTGCTCAGAAAGATGCTGTGAGCTCTCGGAGCA 545

QY 705 CAGTGTGAGCAACGAAATCCAGAGCGGAGTCTTACGCTCCGCTCGGACCAAGCAGC 764
DB 546 CAGTGTGAGCAACGAAATCCAGAGCGGAGTCTTACGCTCCGCTCGGACCAAGCAGC 605

QY 765 GCTGTGCGCTGCGCGCTTGGCCAGCGGAGGCTTTCACGCTTCGAGCCCAAGCTATC 824
DB 606 GCTGTGCGCTGCGCGCTTGGCCAGCGGAGGCTTTCACGCTTCGAGCCCAAGCTATC 665

QY 825 GGTACTGACAGACAGATGACCTTGCCACCCACATCTGTGTGAGAGCGGAGAGC 884
DB 666 GGTACTGACAGACAGATGACCTTGCCACCCACATCTGTGTGAGAGCGGAGAGC 725

QY 885 CCCACCTTACGAGGCGCCCTG 906
DB 726 CCCACCTTACGAGGCGCCCTG 747

RESULT 36
AX011709 812 bp DNA linear PAT 06-SEP-2000
LOCUS AX011709
DEFINITION Sequence 107 from Patent WO9955858.
ACCESSION AX011709
VERSION AX011709.1 GI:9998233
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
REFERENCE 1
AUTHORS Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and Pilarsky,C.
TITLE Human nucleic acid sequences obtained from pancreas tumor tissue
JOURNAL Patient: WO 9955858-A/107 04-NOV-1999;
COMMENT SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN
(DE); PILARSKY CHRISTIAN (DE)
Key Location/Qualifiers
FT source 1..812
FT location/Qualifiers
1..812
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 20.5%; Score 271; DB 6; Length 812;
Best Local Similarity 99.7%; Pred. No. 3.4e-123;
Matches 321; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 585 TCAGTGTCTGTGAGGCACTACAGCTGTCTGCAAGTCTTTCATCAAGCGGACAGCC 644
DB 426 TCAGTGTCTGTGAGGCACTACAGCTGTCTGCAAGTCTTTCATCAAGCGGACAGCC 485

QY 645 AGGGGCGGAGGAGGAGATGCTCTGCTCAGAAAGATGCTGTGAGCTCTCGGAGCA 704
DB 486 AGGGGCGGAGGAGGAGATGCTCTGCTCAGAAAGATGCTGTGAGCTCTCGGAGCA 545

QY 705 CAGTGTGAGCAACGAAATCCAGAGCGGAGTCTTACGCTCCGCTCGGACCAAGCAGC 764
DB 546 CAGTGTGAGCAACGAAATCCAGAGCGGAGTCTTACGCTCCGCTCGGACCAAGCAGC 605

QY 765 GCTGTGCGCTGCGCGCTTGGCCAGCGGAGGCTTTCACGCTTCGAGCCCAAGCTATC 824
DB 606 GCTGTGCGCTGCGCGCTTGGCCAGCGGAGGCTTTCACGCTTCGAGCCCAAGCTATC 665

QY 825 CGTACTGACAGACGAGATCCGCTCCACCCACCATCTCGCTGTCAGACGGGGAGAGC 884
 DB 666 CGTACTGACAGACGAGATCCGCTCCACCCACCATCTCGCTGTCAGACGGGGAGAGC 725
 QY 885 CCGGACCCCTACGAGGGGCCCTG 906
 DB 726 CCGGACCCCTACGAGGGGCCCTG 747

RESULT 37

LOCUS CQ976479 310 bp DNA linear PAT 19-JAN-2005
 DEFINITION Sequence 170 from Patent WO2004113571.
 ACCESSION CQ976479
 VERSION CQ976479.1 GI:57975807
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1
 AUTHORS Einstein, R., McGowan, K.M. and Pando, M.P.
 TITLE Prostate specific genes and the use thereof as targets for prostate
 JOURNAL cancer therapy and diagnosis
 Patent: WO 2004113571-A 170 29-DEC-2004;
 Exonhit Therapeutics S.A. (FR)

FEATURES
 source 1..310
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 15.8%; Score 209; DB 6; Length 310;
 Best Local Similarity 100.0%; Pred. No. 2.5e-92;
 Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 522 CCGAGCTGAGTTTGTTCAGATCATCATCGTGTGTGATGATGATGATGATGATG 581
 DB 102 CCGAGCTGAGTTTGTTCAGATCATCATCGTGTGTGATGATGATGATGATGATG 161
 QY 582 TGATCAGTGCCTGCTGAGCCACTACAGCTGTCTGACGGTCTTCATCAGCCGAC 641
 DB 162 TGATCAGTGCCTGCTGAGCCACTACAGCTGTCTGACGGTCTTCATCAGCCGAC 221
 QY 642 GCCAGGGGGGAGAGAGAGATGCCCTGCTCAGAGAGATGCCGTGGCCCTCGGAGA 701
 DB 222 GCCAGGGGGGAGAGAGAGATGCCCTGCTCAGAGAGATGCCGTGGCCCTCGGAGA 281
 QY 702 GCACAGTGTCAAGCAACGGAATCCAGAG 730
 DB 282 GCACAGTGTCAAGCAACGGAATCCAGAG 310

RESULT 38
 LOCUS CQ976481 529 bp DNA linear PAT 19-JAN-2005
 DEFINITION Sequence 172 from Patent WO2004113571.
 ACCESSION CQ976481
 VERSION CQ976481.1 GI:57975809
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1
 AUTHORS Einstein, R., McGowan, K.M. and Pando, M.P.
 TITLE Prostate specific genes and the use thereof as targets for prostate
 JOURNAL cancer therapy and diagnosis
 Patent: WO 2004113571-A 172 29-DEC-2004;
 Exonhit Therapeutics S.A. (FR)

FEATURES

source Location/Qualifiers
 1..529
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 15.8%; Score 209; DB 6; Length 529;
 Best Local Similarity 100.0%; Pred. No. 2.5e-92;
 Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 522 CCGAGCTGAGTTTGTTCAGATCATCATCGTGTGTGATGATGATGATGATGATG 581
 DB 209 CCGAGCTGAGTTTGTTCAGATCATCATCGTGTGTGATGATGATGATGATGATG 150
 QY 582 TGATCAGTGCCTGCTGAGCCACTACAGCTGTCTGACGGTCTTCATCAGCCGAC 641
 DB 149 TGATCAGTGCCTGCTGAGCCACTACAGCTGTCTGACGGTCTTCATCAGCCGAC 90
 QY 642 GCCAGGGGGGAGAGAGATGCCCTGCTCAGAGAGATGCCGTGGCCCTCGGAGA 701
 DB 89 GCCAGGGGGGAGAGAGATGCCCTGCTCAGAGAGATGCCGTGGCCCTCGGAGA 30
 QY 702 GCACAGTGTCAAGCAACGGAATCCAGAG 730
 DB 29 GCACAGTGTCAAGCAACGGAATCCAGAG 1

RESULT 39

LOCUS CQ976478 579 bp DNA linear PAT 19-JAN-2005
 DEFINITION Sequence 169 from Patent WO2004113571.
 ACCESSION CQ976478
 VERSION CQ976478.1 GI:57975806
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1
 AUTHORS Einstein, R., McGowan, K.M. and Pando, M.P.
 TITLE Prostate specific genes and the use thereof as targets for prostate
 JOURNAL cancer therapy and diagnosis
 Patent: WO 2004113571-A 169 29-DEC-2004;
 Exonhit Therapeutics S.A. (FR)

FEATURES

source 1..579
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 15.8%; Score 209; DB 6; Length 579;
 Best Local Similarity 100.0%; Pred. No. 2.5e-92;
 Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 522 CCGAGCTGAGTTTGTTCAGATCATCATCGTGTGTGATGATGATGATGATGATG 581
 DB 371 CCGAGCTGAGTTTGTTCAGATCATCATCGTGTGTGATGATGATGATGATGATG 430
 QY 582 TGATCAGTGCCTGCTGAGCCACTACAGCTGTCTGACGGTCTTCATCAGCCGAC 641
 DB 431 TGATCAGTGCCTGCTGAGCCACTACAGCTGTCTGACGGTCTTCATCAGCCGAC 490
 QY 642 GCCAGGGGGGAGAGAGATGCCCTGCTCAGAGAGATGCCGTGGCCCTCGGAGA 701
 DB 491 GCCAGGGGGGAGAGAGATGCCCTGCTCAGAGAGATGCCGTGGCCCTCGGAGA 550
 QY 702 GCACAGTGTCAAGCAACGGAATCCAGAG 730
 DB 551 GCACAGTGTCAAGCAACGGAATCCAGAG 579

LOCUS	CO976480	301 bp	DNA	linear	PAT 19-JAN-2005
LOCUS	CO976480	301 bp	DNA	linear	PAT 19-JAN-2005
DEFINITION	Sequence 171 from Patent WO2004113571.				
ACCESSION	CO976480				
VERSION	CO976480.1	GI:57975808			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE	Homo sapiens				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
TITLE	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
JOURNAL	Hominidae; Homo.				
FEATURES	1 Einstein, R., McGowan, K.M. and Pando, M.P. Prostate specific genes and the use thereof as targets for prostate cancer therapy and diagnosis Patent: WO 2004113571-A 171-29-DEC-2004; Exonhit Therapeutics S.A. (FR) Location/Qualifiers 1..301 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"				
ORIGIN					
Query Match	11.5%;	Score 152;	DB 6;	Length 301;	
Best Local Similarity	100.0%;	Pred. No. 5.9e-64;			
Matches 152;	Conservative	0;	Mismatches 6;	Indels 0;	Gaps 0;
Qy	522 CGAGCTGAGATTGTCAGATCATCATCATCATCGTGTGTGTGATGATGATGATGATG 581				
Db	152 CGAGCTGAGATTGTCAGATCATCATCATCATCGTGTGTGTGATGATGATGATGATG 93				
Qy	582 TGATCAGCTGCTGTGTGACCACTACCAAGCTGTCTGACGGTCTTCATCAGCCGAC 641				
Db	92 TGATCAGCTGCTGTGTGACCACTACCAAGCTGTCTGACGGTCTTCATCAGCCGAC 33				
Qy	642 GCCAGGGGCGGAGGAGAGAGATGCGCTGTC 673				
Db	32 GCCAGGGGCGGAGGAGAGATGCGCTGTC 1				
RESULT 41					
LOCUS	CO9735730	270 bp	DNA	linear	PAT 03-FEB-2004
DEFINITION	Sequence 21664 from Patent WO02068579.				
ACCESSION	CO9735730				
VERSION	CO9735730.1	GI:42328620			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE	Homo sapiens				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
TITLE	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
JOURNAL	Hominidae; Homo.				
FEATURES	1 Venter, C.J., Adams, M.C., Li, P.W. and Myers, B.W. Kits, such as nucleic acid arrays, comprising a majority of humanecons or transcripts, for detecting expression and other uses thereof Patent: WO 02068579-A 21664 06-SEP-2002; PE Corporation (NY) (US) Location/Qualifiers 1..270 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"				
ORIGIN					
Query Match	8.3%;	Score 110;	DB 6;	Length 270;	
Best Local Similarity	100.0%;	Pred. No. 4.7e-43;			
Matches 110;	Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

OY		413	ATGACCGCTTGAATGGGGGTCAACAGACCGCCGCCGCCGCCGCAGCCAAATGTC	472
Db		1	ATGACCGCTTGAATGGGGGTCAACAGACCGCCGCCGCCGCCGCAGCCAAATGTC	60
OY		473	TCTTGACAAGTGCACACTGCAAAACGCTCTTTGTTCCAGAGCATGAGATCAC	522
Db		61	TCTTGACAAGTGCACACTGCAAAACGCTCTTTGTTCCAGAGCATGAGATCAC	110
RESULT 42				
COS43985				
LOCUS				
DEFINITION			Sequence 13620 from Patent WO0210449.	
ACCESSION			COS43985	
VERSION			COS43985.1	
KEYWORDS				
SOURCE				
ORGANISM			Homo sapiens (human)	
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
			Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
			Homidae; Homo.	
REFERENCE				
AUTHORS			Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.	
TITLE			Oligonucleotide library for detecting rna transcripts and splice	
JOURNAL			variants that populate a transcriptome	
			Patent: WO 0210449-A 13620 07-FEB-2002;	
FEATURES			CompuGen Inc. (US)	
source			Location/Qualifiers	
			1..60	
			/organism="Homo sapiens"	
			/mol_type="unassigned DNA"	
			/db_xref="taxon:9606"	
ORIGIN				
Query Match			4.5%; Score 60; DB 6; Length 60;	
Best Local Similarity			100.0%; Pred. No. 3.7e-18;	
Matches			60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY		1225	CGCAGCCATCTGAGAACAAAGAGAAGATTAACAGAAAGACACCCTCTTAGGCTCCCCA	12844
Db		1	CGCAGCCATCTGAGAACAAAGAGAAGATTAACAGAAAGACACCCTCTTAGGCTCCCCA	60
RESULT 43				
COS436367/c				
LOCUS				
DEFINITION			CR956367 158243 bp DNA linear HTG 06-AUG-2005	
ACCESSION			CR956367	
VERSION			CR956367.4	
KEYWORDS			HTG; HTGS_PHASEL; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.	
SOURCE			Sus scrofa (pig)	
ORGANISM			Sus scrofa	
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
			Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;	
			Sub.	
			1 (bases 1 to 158243)	
REFERENCE				
AUTHORS			Harley,J.	
TITLE			Direct Submission	
JOURNAL			Submitted (05-AUG-2005) Wellcome Trust Sanger Institute, Hinxton,	
			Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk	
			On Jul 9, 2005 this sequence version replaced gi:68659251.	
COMMENT			----- Genome Center	
			Center: Wellcome Trust Sanger Institute	
			Center code: SC	
			Web site: http://www.sanger.ac.uk	
			Contact: vegas@sanger.ac.uk	
			----- Project Information	
			Center project name: br122c21	
			----- Summary Statistics	
			Assembly program: XGAP4; version 4.5	
			Chemistry: Dye-terminator; 100% of reads	

Query Match	3.9%	Score 51	DB 6	Length 51
Best Local Similarity	100.0%	Pred. No. 1.1e-13		
Matches 51	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Db	1	CACGGTCTTTCATCAGCCCGCACACGCCAGGGGCGGAGAGAGAAATGCCCC	668	
RESULT 46				
LOCUS	BD272547	411 bp	DNA	linear
DEFINITION	Secreted proteins and nucleic acids encoding them.			PAT 17-JUL-2003
ACCESSION	BD272547			
VERSION	BD272547.1	GI:33082315		
KEYWORDS	JP 2002539773-A/56.			
SOURCE	Mus sp.			
ORGANISM	Mus sp.			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 (bases 1 to 411)			
TITLE	Barnes,T.M., Holtzman,D.A., Sharp,J.D. and Frazer,C.C.			
JOURNAL	Secreted proteins and nucleic acids encoding them			
COMMENT	Patent: JP 2002539773-A 56 26-NOV-2002;			
	MILLENNIUM PHARMACEUTICALS INC			
	OS Mus sp. (mouse)			
	PN JP 2002539773-A/56			
	PD 26-NOV-2002			
	PP 01-MAR-2000 JP 2000602247			
	PR 01-MAR-1999 US 60/122458			
	PI THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CHRISTOPHER C PI FRASER			
	PC C12N15/09, C07K14/47, C07K16/18, C12N5/10, C12P21/02, C12Q1/68, PC G01N33/15.			
	PC G01N33/50, G01N33/53, G01N33/56, C12N15/00, C12N5/00 CC			
	Secreted proteins and nucleic acids encoding them			FR Key
FEATURES				
source	FT	Location/Qualifiers		
	FT	1..411		
	location/Qualifiers	1..411		
	/organism="Mus sp."			
	/mol_type="genomic DNA"			
	/db_xref="taxon:10095"			
ORIGIN				
Query Match	3.3%	Score 44	DB 6	Length 411
Best Local Similarity	100.0%	Pred. No. 3.4e-10		
Matches 44	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Db	875	GGGGAGAGAGCCCCCAGCCCTACGAGGAGGCCCTCACCCTCCAGCT	918	
	271	GGGGAGAGAGCCCCCAGCCCTACGAGGAGGCCCTCACCCTCCAGCT	314	
RESULT 47				
LOCUS	BD272546	484 bp	DNA	linear
DEFINITION	Secreted proteins and nucleic acids encoding them.			PAT 17-JUL-2003
ACCESSION	BD272546			
VERSION	BD272546.1	GI:33082314		
KEYWORDS	JP 2002539773-A/55.			
SOURCE	Mus sp.			
ORGANISM	Mus sp.			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 (bases 1 to 484)			
TITLE	Barnes,T.M., Holtzman,D.A., Sharp,J.D. and Frazer,C.C.			
JOURNAL	Secreted proteins and nucleic acids encoding them			
	Patent: JP 2002539773-A 55 26-NOV-2002;			
	MILLENNIUM PHARMACEUTICALS INC			

COMMENT	OS Mus sp. (mouse) PN JP 2002539773-A/55 PD 26-NOV-2002 PF 01-MAR-2000 JP 2000602247 PR 01-MAR-1999 US 60/122458 PI THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CHRISTOPHER C FRASER PC C12N15/09, C07K14/47, C07K16/18, C12N5/10, C12P21/02, C12Q1/68, PC G01N33/15, PC G01N33/50, G01N33/53, G01N33/53, G01N33/566, C12N15/00, C12N5/00 CC
FEATURES	source FT key Location/Qualifiers FT CDS (3) . (413) FT misc_feature (1) . (484). FT Location/Qualifiers 1. .484 /organism="Mus sp." /mol_type="genomic DNA" /db_xref="taxon:10095"
ORIGIN	
Query Match	3.3%; Score 44; DB 6; Length 484;
Best Local Similarity	100.0%; Pred. No. 3,4e-10;
Matches	44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	875 GGGAGAGACCCCACTTACAGAGGCGCCCTGCACCTCCAGCT 918 273 GGGAGAGAGCCCACTTACAGAGGCGCCCTGCACCTCCAGCT 316
RESULT 48	
BD272535	
LOCUS	BD272535 648 bp DNA linear PAT 17-JUL-2003
DEFINITION	Secreted proteins and nucleic acids encoding them.
ACCESSION	BD272535
VERSION	BD272535.1 GI:33082303
KEYWORDS	JP 2002539773-A/44.
SOURCE	Mus sp.
ORGANISM	Mus sp. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciuromorphi; Muridae; Murinae; Mus. 1 (bases 1 to 648) Barnes,T.M., Holtzman,D.A., Sharp,J.D. and Fraser,C.C. Secreted proteins and nucleic acids encoding them Patent: JP 2002539773-A 44 26-NOV-2002; MILLENNIUM PHARMACEUTICALS INC
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	OS Mus sp. (mouse) PN JP 2002539773-A/44 PD 26-NOV-2002 PF 01-MAR-2000 JP 2000602247 PR 01-MAR-1999 US 60/122458 PI THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CHRISTOPHER C FRASER PC C12N15/09, C07K14/47, C07K16/18, C12N5/10, C12P21/02, C12Q1/68, PC G01N33/15, PC G01N33/50, G01N33/53, G01N33/53, G01N33/566, C12N15/00, C12N5/00 CC
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Db 265 GGGGAGAGCCCCCACCCTACCGAGGCCCCCTGCACCTCCAGCT 308

RESULT 49
BD272505 651 bp DNA linear PAT 17-JUL-2003
DEFINITION Secreted proteins and nucleic acids encoding them.
ACCESSION BD272505
VERSION BD272505.1 GI:33082273
KEYWORDS JP 2002539773-A/14.
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 651)
Barnes, T.M., Holtzman, D.A., Sharp, J.D. and Fraser, C.C.
Secreted proteins and nucleic acids encoding them
Patent: JP 2002539773-A 14 26-NOV-2002;
MILLENNIUM PHARMACEUTICALS INC
OS Mus sp. (mouse)
PN JP 2002539773-A/14
PD 26-NOV-2002 JP 200602247
PF 01-MAR-2000 JP 60/122458
PR 01-MAR-1999 US 60/122458
PI THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CHRISTOPHER C
PI FRASER
PC C12N15/09, C07K14/47, C07K16/18, C12N5/10, C12P21/02, C12Q1/68, PC
G01N33/15, G01N33/50, G01N33/53, G01N33/56, G01N33/566, C12N15/00, C12N5/00 CC
Secreted proteins and nucleic acids encoding them FH Key
Location/Qualifiers
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1. 651
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ORIGIN

Query Match 3.3%; Score 44; DB 6; Length 651;
Best Local Similarity 100.0%; Pred. No. 3.4e-10;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 875 GGGGAGAGCCCCCACCCTACCGAGGCCCCCTGCACCTCCAGCT 918
DB 268 GGGGAGAGCCCCCACCCTACCGAGGCCCCCTGCACCTCCAGCT 311

RESULT 50
AF220208 651 bp mRNA linear ROD 05-MAR-2001
LOCUS AF220208
DEFINITION Mus musculus Nedd4 WW domain-binding protein 4 mRNA, partial cds.
ACCESSION AF220208
VERSION AF220208.1 GI:12004973
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 651)
Jolliffe, C.N., Harvey, K.F., Haines, B.P., Parasiyam, G. and Kumar, S.
Identification of multiple proteins expressed in murine embryos as
binding partners for the WW domains of the ubiquitin-protein ligase
Nedd4
Biochem. J. 351 Pt 3, 557-565 (2000)
JOURNAL Biochem. J. 351 Pt 3, 557-565 (2000)
PUBMED 11042109
REFERENCE 2 (bases 1 to 651)
AUTHORS Jolliffe, C.N. and Kumar, S.
TITLE Direct Submission

JOURNAL Submitted (30-DEC-1999) Division of Haematology, Hanson Centre for
Cancer Research, IMVS, Frome Rd, Adelaide, SA 5000, Australia

FEATURES
source Location/Qualifiers
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ORIGIN

Query Match 3.3%; Score 44; DB 9; Length 651;
Best Local Similarity 100.0%; Pred. No. 3.4e-10;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 875 GGGGAGAGCCCCCACCCTACCGAGGCCCCCTGCACCTCCAGCT 918
DB 223 GGGGAGAGCCCCCACCCTACCGAGGCCCCCTGCACCTCCAGCT 266

Search completed: February 28, 2006, 12:45:02
JOD time : 6715 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2006, 09:41:56 ; Search time 800 Seconds
(without alignments)
11005.074 Million cell updates/sec

Title: US-09-934-249-1

Perfect score: 1321
Sequence: 1 cgaccgcgctctcgagcgcg.....ctgcgtagctgaagagcag 1321

Scoring table: OLIGO NUC
Gapop 60.0, Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word-size: 23

Total number of hits satisfying chosen parameters: 3924

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

Database :

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- 2: geneeqn1900s:*
- 3: geneeqn2000s:*
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- 8: geneeqn2003as:*
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- 12: geneeqn2004as:*
- 13: geneeqn2004bs:*
- 14: geneeqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1229	93.0	4839	8	ACC49552 Tumour-as
5	1229	93.0	4839	11	ADP65809 Human STA
6	1229	93.0	4839	11	ADP65729 Human tra
7	1229	93.0	4839	12	ADM67045 Human hom
8	1229	93.0	4839	13	ADM65875 Human pro
9	1229	93.0	4839	13	ADM66778 Human pro
10	1229	93.0	4839	13	ADU06063 Novel bro
11	1229	93.0	4839	14	ADM43368 Prostate
12	1178	89.2	1383	10	ADP37326 Nuclear f
13	909	68.8	4519	13	ADP37454 Pancreat
14	864	65.4	864	11	ADN38809 Cancer/an
15	800	60.6	1140	6	ABK92120 Prostate
16	800	60.6	1140	10	ADM60105 Human and
17	800	60.6	1140	10	ADM62276 Human PME
18	800	60.6	1140	12	ADP39826 Human PME
19	800	60.6	1141	10	ADM75588 Prostate

20	800	60.6	1850	8	ACC49536 Tumour-as
21	800	60.6	4527	11	ADL83313 Human and
22	800	60.6	4527	11	ADV85880 Human ARP
23	800	60.6	4531	14	ABE22833 Human col
24	800	60.6	4538	14	ABE22832 Human col
25	788	59.7	1066	4	AAI57868 Human pol
26	755	57.2	759	10	ADP17545 Human and
27	755	57.2	759	10	ADH62277 Human PME
28	755	57.2	759	12	ADP39827 Human PME
29	749	56.7	969	3	AAH75151 cDNA enco
30	749	56.7	1061	3	AAH47429 Sequence
31	749	56.7	1085	10	ADP37324 Nuclear f
32	749	56.7	1334	8	ABZ6103 Human sec
33	744	56.3	969	3	AAH75163 cDNA clon
34	713	54.0	806	8	ACC49537 Tumour-as
35	698	52.8	969	3	AAH75164 cDNA clon
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37	560	42.4	1583	6	ABH61424 Prostate
38	409	31.0	711	12	ADN98767 Novel hum
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40	401	30.4	408	5	AAH5983
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42	394	29.8	1069	4	AAI59654 Human pol
43	364	27.6	474	10	ABZ84732 Tox1colog
44	302	22.9	693	6	ABK12143 Human MIV
45	271	20.5	812	2	AAZ52964 Human pro
46	229	17.3	254	3	AAH41265 Human sec
47	209	15.8	310	14	ADM43372 Prostate
48	209	15.8	529	14	ADM43371 Prostate
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50	178	13.5	467	9	ACH14862 Human adu
51	152	11.5	301	14	ADM43373 Prostate
52	106	8.0	1879	5	AAH84503 DNA enco
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58	56	4.2	522	13	ADT90182 Human gen
59	56	4.2	522	13	ADT90322 Human gen
60	51	3.9	51	4	AAH89714 Human cod
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63	44	3.3	878	6	ABK12142 Mouse cDN
64	44	3.3	1713	3	AAH75167 cDNA clon
65	44	3.3	1713	3	AAH75166 cDNA clon
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69	42	3.2	673	12	ADG45576 Liver inf
70	42	3.2	673	12	ADH22874 Partial D
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72	37	2.8	837	6	ABQ43498 Oligonuc
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74	34	2.6	640	3	AAH54811 Novel can
75	34	2.6	640	3	AAH54811 Novel can
76	34	2.6	1050	13	AAH56015 Bucalyptu
77	34	2.6	1237	14	ADT18364 Plant cDN
78	34	2.6	1752	11	ADL28297 Eucalyptu
79	34	2.6	2000	8	ADH72533 Rice gene
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93	32	2.4	1964	4	AA113901	Probe #38	c 166	29	2.2	3532	6	AB565219	Ab565219 cDNA enco
94	32	2.4	1964	4	AA555612	Human foe	c 167	29	2.2	4122	7	ADS99915	Ad999915 Human cad
95	32	2.4	1964	4	AA135267	Probe #39	c 168	29	2.2	4122	10	ACC72793	Acc72793 Human can
96	32	2.4	1964	4	ABA45134	Human bre	c 169	29	2.2	4122	11	ADN95504	Adn95504 Human BBC
97	32	2.4	1964	4	ABA25310	Probe #37	c 170	29	2.2	4122	12	ADP26912	Adp26912 Human N-C
98	32	2.4	1964	4	AAK29307	Human bon	c 171	29	2.2	4122	14	AD265970	Ad265970 Human N-C
99	32	2.4	1964	4	AAK03841	Human bra	c 172	29	2.2	4122	14	AE835167	Aeb35167 Human Gef
100	32	2.4	1964	4	ABS28927	Human liv	c 173	29	2.2	4136	5	AA578503	Aad578503 DNA enco
101	32	2.4	1964	4	AA103769	Probe #37	c 174	29	2.2	4595	12	AD024631	Adc24631 Human sof
102	32	2.4	1964	4	ABS03866	Human gen	c 175	29	2.2	5370	4	ABL07877	Ab107877 Drosophi
103	32	2.4	1964	4	ADA72945	Rice gene	c 176	29	2.2	37996	4	ABL07876	Abd33307 Murine ca
104	32	2.4	2000	8	AA56476	Eucalyptu	c 177	29	2.2	53828	13	ABD33307	Abd33307 Murine ca
105	31	2.3	359	3	AA56618	Genomic s	c 178	28	2.1	204	8	ABZ81761	Abz81761 Huntingto
106	31	2.3	533	3	AA56618	Eucalyptu	c 179	28	2.1	251	6	ABV95011	Abv95011 Human pan
107	31	2.3	776	6	AB033408	Oligonuc	c 180	28	2.1	267	14	ADV77136	Adv77136 Huntingto
108	31	2.3	776	6	AB033408	Oligonuc	c 181	28	2.1	321	5	AA13973	Ad13973 Human 5'
109	31	2.3	2332	10	ADB62546	Human CDN	c 182	28	2.1	362	14	ADV77137	Adv77137 Huntingto
110	31	2.3	2808	4	ABL26560	Human foe	c 183	28	2.1	381	4	ABL41662	Ab141662 Nucleotid
111	31	2.3	10437	5	AA541709	Genomic s	c 184	28	2.1	412	8	ABX47996	Abx47996 Bovine ES
112	31	2.3	12620	5	AA581691	Human ner	c 185	28	2.1	504	4	ABL41663	Ab141663 Nucleotid
113	30	2.3	2109	5	AA581691	Human ner	c 186	28	2.1	515	2	AAK18930	Aax18930 Human hun
114	29	2.2	401	4	ABA55787	Human foe	c 187	28	2.1	530	10	ADC46893	Adc46893 Huntingto
115	29	2.2	401	4	ABA55787	Human foe	c 188	28	2.1	584	13	ADU87449	Adu87449 Exon 1 of
116	29	2.2	401	4	AA135443	Probe #41	c 189	28	2.1	600	8	ABZ81778	Abz81778 Huntingto
117	29	2.2	401	4	ABA45299	Human bre	c 190	28	2.1	614	8	ABZ81762	Abz81762 Huntingto
118	29	2.2	401	4	ABA25470	Probe #39	c 191	28	2.1	636	9	ADA49298	Ada49298 Maize gen
119	29	2.2	401	4	AAK29492	Human bon	c 192	28	2.1	636	11	ACL344692	Ad344692 Rice abio
120	29	2.2	401	4	AAK04010	Human bra	c 193	28	2.1	636	12	ADU44871	Ad44871 Plant CDN
121	29	2.2	401	4	AB829116	Human liv	c 194	28	2.1	645	2	AA742476	Aat42476 HuntLA co
122	29	2.2	401	5	AA103921	Probe #39	c 195	28	2.1	700	3	AAA37651	Aaa37651 FMR1 gene
123	29	2.2	401	6	AB804041	Human gen	c 196	28	2.1	729	6	ABQ32810	Abq32810 Oligonuc
124	29	2.2	446	4	AA123276	Probe #13	c 197	28	2.1	732	11	ACL33931	Ac133931 Rice abio
125	29	2.2	446	4	ABA68382	Human foe	c 198	28	2.1	732	11	ACL33931	Ac133931 Rice abio
126	29	2.2	446	4	AA148596	Probe #17	c 199	28	2.1	771	13	ADS92653	Ad92653 Chitinase
127	29	2.2	446	4	ABA50433	Human bre	c 200	28	2.1	771	13	ADS92653	Ad92653 Chitinase
128	29	2.2	446	4	ABA53739	Probe #13	c 201	28	2.1	771	14	ADZ81097	Adz81097 Nucleotid
129	29	2.2	446	4	AAK45259	Human bon	c 202	28	2.1	771	14	ADZ81091	Adz81091 Nucleotid
130	29	2.2	446	4	AAK16757	Human bra	c 203	28	2.1	774	13	ADS92623	Ad92623 Chitinase
131	29	2.2	446	4	AA842140	Human liv	c 204	28	2.1	774	13	ADS92623	Ad92623 Chitinase
132	29	2.2	446	5	AA108921	Probe #89	c 205	28	2.1	774	13	ADS82653	Ad82653 Chitinase
133	29	2.2	446	6	AB816574	Human gen	c 206	28	2.1	774	14	ADZ81087	Adz81087 Nucleotid
134	29	2.2	545	6	ABQ42791	Oligonuc	c 207	28	2.1	774	14	ADZ81113	Adz81113 Nucleotid
135	29	2.2	545	6	ABQ42790	Oligonuc	c 208	28	2.1	774	14	ADZ81057	Adz81057 Nucleotid
136	29	2.2	546	6	ABQ26184	Oligonuc	c 209	28	2.1	777	13	ADS92619	Ad92619 Chitinase
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138	29	2.2	860	12	AD142555	Plant tra	c 211	28	2.1	840	11	ADU12126	Ad12126 Maize CDN
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140	29	2.2	1128	2	AA220594	Human fib	c 213	28	2.1	966	14	ADV77134	Adv77134 Huntingto
141	29	2.2	1128	2	AA220594	Human fib	c 214	28	2.1	1020	8	ABZ81760	Abz81760 Huntingto
142	29	2.2	1406	13	ADS31839	Human fib	c 215	28	2.1	1061	13	AE866996	Aeb66996 Rice geno
143	29	2.2	1466	13	ADU18046	Human can	c 216	28	2.1	1061	13	ADX33157	Adx33157 Plant ful
144	29	2.2	1546	10	AAAD63206	Human DNA	c 217	28	2.1	1077	13	ADX32647	Adx32647 Plant ful
145	29	2.2	1546	11	AAAD62807	Human DNA	c 218	28	2.1	1086	13	ADX48720	Adx48720 Plant ful
146	29	2.2	1546	11	ADP88302	Non-metas	c 219	28	2.1	1106	13	ADX62563	Adx62563 Plant ful
147	29	2.2	1546	12	ADQ49084	Human ded	c 220	28	2.1	1116	14	ADM16398	Adm16398 Eucalyptu
148	29	2.2	1546	13	ADR25099	Breast ca	c 221	28	2.1	1138	13	ADX59637	Adx59637 Plant ful
149	29	2.2	1546	13	ADM88591	Human fib	c 222	28	2.1	1203	2	AAZ00869	Aaz00869 Human c-M
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152	29	2.2	1656	5	ADA48243	Rice gene	c 225	28	2.1	1302	13	ADU15431	Adu15431 Novel hum
153	29	2.2	1835	9	AA578504	Human encod	c 226	28	2.1	1317	13	ACL26768	Ac126768 Rice abio
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156	29	2.2	2853	6	AA885331	DNA enco	c 229	28	2.1	1650	6	ABK89246	Abk89246 Human CAG
157	29	2.2	2853	6	AA885331	DNA enco	c 230	28	2.1	2000	8	ADA71579	Ada71579 Rice gene
158	29	2.2	2853	6	AA885331	DNA enco	c 231	28	2.1	2097	14	AE827093	Aeb27093 Pinus rad
159	29	2.2	2913	5	AA166506	Rat SAPK	c 232	28	2.1	2145	11	ADN95150	Adn95150 Human BEC
160	29	2.2	2987	9	AA166506	Rat SAPK	c 233	28	2.1	2145	13	ADP54614	Adp54614 Human PRO
161	29	2.2	2987	9	AA166506	Rat SAPK	c 234	28	2.1	2145	13	ADP54614	Adp54614 Human PRO
162	29	2.2	3131	12	ADQ19443	Human sof	c 235	28	2.1	2145	14	ADY16190	Ady16190 DNA enco
163	29	2.2	3131	14	ADQ19443	Human sof	c 236	28	2.1	2145	14	ADY16190	Ady16190 DNA enco
164	29	2.2	3366	5	AD162149	Human ova	c 237	28	2.1	2145	14	ADY19857	Ady19857 DNA enco
165	29	2.2	3444	10	AD152508	DNA enco	c 238	28	2.1	2183	2	AAQ28290	Aaq28290 Fragment

239	28	2.1	3765	2	AAQ31890	312	27	2.0	110000	13	ABD32909_0	Abd32909 Mouse can
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241	28	2.1	4246	13	ADR14374	314	27	2.0	154746	6	AAD25519	Aad25519 Human her
242	28	2.1	4246	13	ADP14834	315	26	2.0	50	4	AAH89715	Aah89715 Human cod
243	28	2.1	4246	13	ADP24271	316	26	2.0	171	3	AAA31044	Aaa31044 Plant mic
244	28	2.1	4246	14	ADP24271	317	26	2.0	263	3	AAA31075	Aaa31075 Plant mic
245	28	2.1	4362	6	ABK84641	318	26	2.0	318	3	AAA31182	Aaa31182 Plant mic
246	28	2.1	4362	6	ABK84641	319	26	2.0	367	4	AAFA4741	Aaf44741 ATL2 vari
247	28	2.1	9732	5	AA579690	320	26	2.0	367	10	ADB94928	Adb94928 Programme
248	28	2.1	10348	5	AA579690	321	26	2.0	375	6	ABL80276	AbL80276 Human ova
249	28	2.1	10348	5	AA579690	322	26	2.0	409	4	AAI80936	Aai80936 Human pol
250	28	2.1	10348	5	AA579690	323	26	2.0	445	4	AAK93630	Aak93630 Human CDN
251	28	2.1	10366	2	AAV05828	324	26	2.0	445	4	AAK92100	Aak92100 Human CDN
252	28	2.1	10366	2	AAV05828	325	26	2.0	445	12	ADL28527	AdL28527 5' end of
253	28	2.1	10366	2	AAV05828	326	26	2.0	445	12	ADL30057	AdL30057 3' end of
254	28	2.1	13672	13	ADR24866	327	26	2.0	480	4	AAH46892	Aah46892 CDNA enco
255	28	2.1	13672	13	ADR24866	328	26	2.0	543	12	ACH77806	Ach77806 Human gen
256	28	2.1	13994	12	ADP44619	329	26	2.0	553	10	ADP09617	AdP09617 Human Pat
257	28	2.1	15698	6	ABL34141	330	26	2.0	553	10	ADK58869	AdK58869 Plant DNA
258	28	2.1	27642	4	AAK77486	331	26	2.0	553	10	ADK57385	AdK57385 Plant DNA
259	28	2.1	30611	13	ABD32618	332	26	2.0	567	3	AA229550	Aa229550 HIV codon
260	28	2.0	393	5	AAAF67438	333	26	2.0	567	3	AA229550	Adi42155 Plant tra
261	28	2.0	402	10	AAAD23448	334	26	2.0	570	12	ADP62830	AdP62830 Transcript
262	28	2.0	402	10	ADP62830	335	26	2.0	570	12	ADP62830	AdP62830 Transcript
263	28	2.0	428	6	ABK53867	336	26	2.0	581	6	ABQ15881	AbQ15881 Oligonuc
264	28	2.0	514	6	ABQ32463	337	26	2.0	581	6	ABQ15880	AbQ15880 Oligonuc
265	28	2.0	514	6	ABQ32462	338	26	2.0	603	4	AA530620	Aa530620 DNA enco
266	28	2.0	581	6	ABQ15810	339	26	2.0	603	4	AA530620	Aa530620 DNA enco
267	28	2.0	581	6	ABQ15810	340	26	2.0	603	4	AA530620	Aa530620 DNA enco
268	28	2.0	582	13	ADR31620	341	26	2.0	603	8	ACA03383	AcA03383 Genomic
269	28	2.0	598	12	ADN30328	342	26	2.0	603	9	ADP6731	AdP6731 Novel lun
270	28	2.0	598	12	ADN30328	343	26	2.0	603	10	ADG41362	AdG41362 Human res
271	28	2.0	615	10	AEA05171	344	26	2.0	603	11	ADP97136	AdP97136 Human res
272	28	2.0	820	10	ADP17321	345	26	2.0	621	11	ACL30015	AcL30015 Rice abio
273	28	2.0	820	10	ADP17321	346	26	2.0	621	11	ACL30406	AcL30406 Rice abio
274	28	2.0	820	10	ADP17321	347	26	2.0	621	12	ADJ39281	AdJ39281 Plant CDN
275	28	2.0	820	10	ADP17321	348	26	2.0	641	12	ADL19337	AdL19337 Wheat ser
276	28	2.0	820	10	ADP17321	349	26	2.0	641	12	ADL19337	AdL19337 Wheat ser
277	28	2.0	900	5	AA587781	350	26	2.0	645	10	ADP94844	AdP94844 Programme
278	28	2.0	900	5	AA587781	351	26	2.0	645	10	ADP94844	AdP94844 Programme
279	28	2.0	1041	8	ACC50221	352	26	2.0	646	6	AEQ99078	Aeq99078 Human ORF
280	28	2.0	1041	12	ADN04997	353	26	2.0	656	10	ADK58028	AdK58028 Plant DNA
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282	28	2.0	1041	13	ADP25212	355	26	2.0	718	6	ABQ13576	AbQ13576 Oligonuc
283	28	2.0	1119	10	ADB78916	356	26	2.0	753	6	ABQ39707	AbQ39707 Oligonuc
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287	28	2.0	1161	12	ACL26493	360	26	2.0	776	6	ABQ17567	AbQ17567 Oligonuc
288	28	2.0	1161	12	ACL26493	361	26	2.0	776	6	ABQ17567	AbQ17567 Oligonuc
289	28	2.0	1373	3	AA258981	362	26	2.0	777	13	ADK51803	AdK51803 Plant ful
290	28	2.0	1403	4	AA158073	363	26	2.0	777	13	ADK51803	AdK51803 Plant ful
291	28	2.0	1403	4	AA158073	364	26	2.0	780	11	ACL30016	AcL30016 Rice abio
292	28	2.0	1444	4	AA159859	365	26	2.0	854	6	ABQ31174	AbQ31174 Oligonuc
293	28	2.0	1587	4	ABA09559	366	26	2.0	854	6	ABQ31174	AbQ31174 Oligonuc
294	28	2.0	1587	4	ABA09559	367	26	2.0	861	11	ACL30396	AcL30396 Rice abio
295	28	2.0	1720	14	ADP16415	368	26	2.0	861	11	ACL30396	AcL30396 Rice abio
296	28	2.0	2000	8	ADA73300	369	26	2.0	870	11	ACL26178	AcL26178 Rice abio
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301	28	2.0	2384	10	ADG32894	374	26	2.0	938	11	ACL38937	AcL38937 Rice abio
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303	28	2.0	2498	10	ADA53201	376	26	2.0	1040	13	ADK23126	AdK23126 Plant ful
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305	28	2.0	3110	3	AAH10672	378	26	2.0	1121	13	ADT19718	AdT19718 Plant CDN
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310	28	2.0	8615	5	ABAI4693	383	27	2.0	1197	3	AA257859	Aa257859 Protein r
311	28	2.0	8615	5	ABAI4693	384	27	2.0	1227	14	ABE66604	AbE66604 Rice geno


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Adu02022 Novel hum
Ada69463 Rice gene
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Ach91938 Human gen
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Abq22357 Oligonuc1
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Adp79328 Human cas
Adx07095 Cyc1in-de
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Adq87148 Human tum
Adq84862 Human tum
Adx07289 Cyc1in-de
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Aak52560 Human pol
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Aak94415 Human ful
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ALIGNMENTS

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RESULT 1
ID ABEK12137 standard; cDNA: 1321 BP.
XX ABEK12137;
AC ABEK12137;
XX 05-JUN-2002 (first entry)
XX Human cDNA encoding Mechanically Induced Vascular Receptor 1, MIVR-1.
DE Human; sr; gene; MIVR-1; Mechanically Induced Vascular Receptor 1;
XX cytoskeletal; cardiant; cerebroprotective; antiarteriosclerotic;
XX cardiac cell; anti-apoptotic; vascular endothelial cell;
XX cardiac hypertrophy; myocardial infarction; stroke; arteriosclerosis;
XX heart failure.
XX Homo sapiens.
XX Key 413..1276
XX CDS /product= "MIVR-1"
XX /note= "This region is specifically claimed in claim 3"
XX PN WO200216416-A2.
```


XX 28-FEB-2002.
 XX 21-AUG-2001; 2001WO-US026089.
 XX 22-AUG-2000; 2000US-0227159P.
 XX (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
 XX (PFIZ) PFIZER INC.
 XX Lee RT, Landeschulz KT, Kennedy SP, Thompson JF, Turi TG;
 XX MPI: 2002-280912/32.
 XX P-PSDB; AAU78231.
 XX Novel nucleic acid molecule encoding Mechanically Induced Vascular
 XX Receptor-1 polypeptide, useful for treating cardiovascular diseases.
 XX Claim 2; Page 87-88; 105pp; English.
 XX The invention relates to an isolated nucleic acid molecule encoding a
 XX Mechanically Induced Vascular Receptor (MIVR)-1 polypeptide having
 XX cardiac cell anti-apoptotic activity and fragments of it provided they
 XX are not identical to Genbank sequences AT761441.1, AT594390, NM 004338
 XX and A0177461. Also included are expression vectors, host cells, the MIVR-
 XX 1 polypeptide, MIVR-1 binding peptides, modulators of MIVR-1, contacting
 XX a molecule having cardiac cell anti-apoptotic activity with a candidate
 XX agent, where the molecule is a nucleic acid molecule comprising MIVR-1,
 XX IEX-1, VDU-1, BNG-2 and TIS-11d or its expression product, determining
 XX if the anti-apoptotic activity is modulated and thereby identifying a
 XX modulator. The cardiac cell anti-apoptotic molecules and nucleic acids
 XX of the invention are useful for treating, diagnosing and monitoring
 XX progression of such diseases and disorders as characterised by increased
 XX apoptotic cell-death of vascular endothelial cells e.g. cardiac
 XX hypertrophy, myocardial infarction, stroke, arteriosclerosis and heart
 XX failure. The present sequence encodes human MIVR-1
 XX
 XX Sequence 1321 BP; 223 A; 493 C; 440 G; 165 T; 0 U; 0 Other;

Query Match 100.0%; Score 1321; DB 6; Length 1321;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGACCGCGGTCTCGAGCGAAACCGGATCTCTTGAGCTTGATGAGAGAGAGCGG 60
 DB 1 CGACCGCGGTCTCGAGCGAAACCGGATCTCTTGAGCTTGATGAGAGAGAGCGG 60
 QY 61 CGGCG 120
 DB 61 CGGCG 120
 QY 121 GCGCGGAGCG 180
 DB 121 GCGCGGAGCG 180
 QY 121 GCGCGGAGCG 180
 DB 121 GCGCGGAGCG 180
 QY 181 AGCG 240
 DB 181 AGCG 240
 QY 241 TGAAGCG 300
 DB 241 TGAAGCG 300
 QY 301 CTGCG 360
 DB 301 CTGCG 360
 QY 361 CCG 420
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DB 421 CTTGATGGGGGTAAACAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
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 DB 481 GTGGAAGTGAAGGCTTTGTTCCAGAGCATGAGATCAAGGAGCTGAGTTGTTCA 540
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 DB 841 GATGACCTGACATCCACATCTGTGTGACAGAGGAGAGGAGGAGGAGGAGGAGG 900
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 QY 1021 CCG 1080
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 DB 1261 AGGACACCTCTCTAGAGGTTCCAGAGGAGGCGCGCGCGCGCGCGCGCGCGCG 1320
 QY 1321 G 1321
 DB 1321 G 1321

RESULT 2
 AEB22787
 ID AEB22787 standard; DNA; 4930 BP.
 XX AEB22787;
 AC 22-SEP-2005 (first entry)
 XX Human colon cancer-associated gene SEQ ID NO:82.
 DE

DB 1141 AGTGGGCGGCTCTTCTGTGAGGGGACCCGGCTCCACACACACATCGGCCCTTA 1200
QY 1220 GAGAGCGCAGCATCTGAGAGCAAGAGATMAAAGAGAGACACCTCTCTAGGGT 1279
DB 1201 GAGAGCGCAGCATCTGAGAGCAAGAGATMAAAGAGAGACACCTCTCTAGGGT 1260
QY 1280 CCCGAGGGGGCGGGGCTGGGGCTGCGTAGGTGAAGAGGCGAG 1321
DB 1261 CCCGAGGGGGCGGGGCTGGGGCTGCGTAGGTGAAGAGGCGAG 1302

RESULT 3
ID ACN40804 standard; cDNA; 4911 BP.
ACN40804;
ACN40804;
18-NOV-2004 (first entry)
Tumour-associated antigenic target (TAT) cDNA DNA326860, SEQ ID NO:5823.
Tumour-associated antigenic target; TAT; human; overexpression; cancer;
tumour; diagnosis; cell proliferative disorder; breast cancer;
colorectal cancer; lung cancer; ovarian cancer; liver cancer;
central nervous system cancer; bladder cancer; pancreatic cancer;
cervical cancer; melanoma; leukaemia; hybridisation probe;
chromosome identification; chromosome mapping; gene mapping;
gene therapy; cytostatic; gene; ss.
Homo sapiens.
WO2004030615-A2.
15-APR-2004.
29-SEP-2003; 2003WO-US028547.
02-OCT-2002; 2002US-0414971P.
(GENTH) GENEINTECH INC.
Wu TD, Zhang Z, Zhou Y;
WPI; 2004-347921/32.
New tumor-associated antigenic target polypeptides and nucleic acids,
useful in preparing a medicament for treating or detecting a
proliferative disorder, e.g. breast, lung, colorectal, ovarian or
prostate cancer or tumor.
Claim 1; SEQ ID NO 5823; 7273pp; English.

The invention relates to human tumour-associated antigenic target (TAT)
polypeptides, and their related nucleic acids. The TAT polypeptides are
overexpressed in cancer tissues compared to normal tissues, and may thus
serve as effective targets for the diagnosis and treatment of cancer in
mammals. The invention also relates to nucleic acid and polypeptide
sequences at least 80% identical to the TAT nucleic acids and
polypeptides; expression vectors and host cells comprising a TAT nucleic
acid; an antibody specific for a TAT polypeptide; a peptide or organic
molecule which binds to a TAT polypeptide; fusion proteins comprising a
TAT polypeptide; and methods and compositions for the treatment or
diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
antibodies, antagonists, binding molecules and compositions are useful
for diagnosing or treating a cell proliferative disorder associated with
increased TAT expression, particularly cancers such as breast cancer,
colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
cancer, pancreatic cancer, cervical cancer, cancers of the central
nervous system, melanoma and leukaemia. TAT nucleic acids may further be
used as hybridisation probes, in chromosome and gene mapping, in
chromosome identification and in gene therapy. The present sequence
represents a TAT nucleic acid of the invention

XX Sequence 4911 BP; 1114 A; 1331 C; 1324 G; 1142 T; 0 U; 0 Other;
SQ Query Match 96.5%; Score 1301; DB 13; Length 4911;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 AACCCGATCTCTTGAATGATGAGAGAGAGAGGCGGCGGCGGCGGCGGAG 80
DB 1 AACCCGATCTCTTGAATGATGAGAGAGAGAGGCGGCGGCGGCGGCGGAG 60
QY 81 GCGCTCGGCTGGGAGAAAGCTAGCGGAGAGGCTAGCCCGCGGAGCGGCGGCGG 140
DB 61 GCGCTCGGCTGGGAGAAAGCTAGCGGAGAGGCTAGCCCGCGGAGCGGCGGCGG 120
QY 141 TGGCAGCCCATTTTCGAGCGCCACCGCGGGGCACTGCGGACGCCCCCGGGGCTGGCGAG 200
DB 121 TGGCAGCCCATTTTCGAGCGCCACCGCGGGGCACTGCGGACGCCCCCGGGGCTGGCGAG 180
QY 201 GGGAGGCGGGGGGGGGCGGAGGCGGCGGCGGCGGCACTGAGGCGGCGGCGGCGG 260
DB 181 GGGAGGCGGGGGGGGGCGGAGGCGGCGGCGGCGGCACTGAGGCGGCGGCGGCGG 240
QY 261 GAACCTTGGCGGCGAGCCCGAGCCCGGAGCCCGGAGCCCGGCGGCGGCGGCGGCTCC 320
DB 241 GAACCTTGGCGGCGAGCCCGAGCCCGGAGCCCGGAGCCCGGCGGCGGCGGCGGCTCC 300
QY 321 TGCATGCGGGGCGCCAGCTCCGGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 380
DB 301 TGCATGCGGGGCGCCAGCTCCGGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
QY 381 CCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 440
DB 361 CCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
QY 441 CCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTT 500
DB 421 CCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTT 480
QY 501 TGTTCAGAGCAGTGAAGATCAAGAGCTGAGGTTGTTCAATCATCATCTGTTGG 560
DB 481 TGTTCAGAGCAGTGAAGATCAAGAGCTGAGGTTGTTCAATCATCATCTGTTGG 540
QY 561 TGATATATGTATGTGTGTGTGTATCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 620
DB 541 TGATATATGTATGTGTGTGTGTGTATCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
QY 621 GGTCTTTCATCAGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 680
DB 601 GGTCTTTCATCAGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
QY 681 GATGCTGTGTGCGCTCGAGAGCAGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 740
DB 661 GATGCTGTGTGCGCTCGAGAGCAGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
QY 741 AGCGCCCGCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 800
DB 721 AGCGCCCGCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 780
QY 801 TCCACCGCTTCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 860
DB 781 TCCACCGCTTCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 840
QY 861 TCTGCTGTGACAGCGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 920
DB 841 TCTGCTGTGACAGCGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 900
QY 921 GGGAGCCCGGAGCAGGCTGGAATCTGAATCCGGGAATCGGTGGCGGCAACCCCAACAGAA 980
DB 901 GGGAGCCCGGAGCAGGCTGGAATCTGAATCCGGGAATCGGTGGCGGCAACCCCAACAGAA 960
QY 981 CCATCTTGACAGTGAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1040

Db 961 CCATCTTCGACGATGACCTGATGATGTCACAGGCTGGGGCCCTGCCCCCAGCA 1020
Qy 1041 GTACTCGGGGATCAAGCCCACTGCTACGGCAGCGGGGGCGATGAGAGGGGCGCGC 1100
Db 1021 GTACTCGGGGATCAAGCCCACTGCTACGGCAGCGGGGGCGATGAGAGGGGCGCGC 1080
Qy 1101 CCACCTACAGGAGGATCTGAGGCACTACCGGGGCTCTCTTCAGAGCAGAGAGCA 1160
Db 1081 CCACCTACAGGAGGATCTGAGGCACTACCGGGGCTCTCTTCAGAGCAGAGAGCA 1140
Qy 1161 GTGGGCGCGCTCTCTGCTGAGAGGAGCCGGCTTCACACACACATCGCGCTTAG 1220
Db 1141 GTGGGCGCGCTCTCTGCTGAGAGGAGCCGGCTTCACACACACATCGCGCTTAG 1200
Qy 1221 AGACCGGAGCCTATCTGAGGCAAGAGATTAACAGAGAGCACCCTCTAGAGGTC 1280
Db 1201 AGACCGGAGCCTATCTGAGGCAAGAGATTAACAGAGAGCACCCTCTAGAGGTC 1260
Qy 1281 CCCAGGGGGGCGGGGCTGGGCTGGGAGTGAAGAGGAG 1321
Db 1261 CCCAGGGGGGCGGGGCTGGGCTGGGAGTGAAGAGGAG 1301

RESULT 4
ACC49552
ID ACC49552 standard; cDNA; 4839 BP.
ACCA9552;
01-JUL-2003 (first entry)
Tumour-associated antigenic target protein TA7379 SEQ ID NO:119.
Human; tumour-associated antigenic target; TAT; tumour; diagnosis;
Cancer; gene; ss.
Homo sapiens.
WO2003024392-A2.
27-MAR-2003.
11-SEP-2002; 2002MO-US028859.
18-SEP-2001; 2001US-0322268P.
19-OCT-2001; 2001US-0339227P.
07-NOV-2001; 2001US-0336827P.
20-NOV-2001; 2001US-0331906P.
02-JAN-2002; 2002US-0345444P.
03-APR-2002; 2002US-0369724P.
19-AUG-2002; 2002US-0404809P.
(GETH) GENENTECH INC.
Frentz G, Hillan KJ, Philippe HS, Polakis P, Spencer SD,
Williams PM, Wu TD, Zhang Z;
WPI; 2003-354551/33.
P-PSDB; ABP97234.
New antibodies against tumor-associated antigenic target polypeptide,
useful for treating or diagnosing tumors or cancers in mammals e.g.
prostate cancer, lung cancer, prostate adenocarcinomas or renal cell
carcinomas.
Claim 2; Fig 119; 285bp; English.
ACC49493 to ACC49552 encode the human tumour-associated antigenic target
(TAT) proteins given in ABP97175 to ABP97234. The present invention
describes an isolated antibody that binds to a polypeptide having at
least 80 % sequence identity to any of the 60 150-800 residue amino acid
sequences (S1), given in ABP97175 to ABP97234, comprising (S1), lacking
its associated signal peptide, encoded by any of the 60 2000-3000 base

CC pair sequences (S2), given in ACC49493 to ACC49552. TAT proteins have
CC cytostatic activity. The antibody can be used for treating or diagnosing
CC tumours or cancers in mammals, e.g. prostate cancer, lung cancer, breast
CC cancer, colon cancer, ovarian cancer, prostate adenocarcinomas, renal
CC cell carcinomas, or thyroid cancer
XX
SQ Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;
Query Match 93.0%; Score 1229; DB 8; Length 4839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 93 GAAAGCTAGCGGAGAGGCTCAAGCCCGGCGGAGCGCGCCGCTGCCAGCCATT 152
Db 1 GAAAGCTAGCGGAGAGGCTCAAGCCCGGCGGAGCGCGCCGCTGCCAGCCATT 60
Qy 153 TTCCGAGCGCCACCCTGGGCACTGCCAGCGCCCTCGGGCTGCTCGAGGGAGGCGGG 212
Db 61 TTCCGAGCGCCACCCTGGGCACTGCCAGCGCCCTCGGGCTGCTCGAGGGAGGCGGG 120
Qy 213 GGGGCGAGGAGGCGGCTCCCGGCACTGAGCCCGGCGGCGGCGGAACTTGGCGGC 272
Db 121 GGGGCGAGGAGGCGGCTCCCGGCACTGAGCCCGGCGGCGGCGGAACTTGGCGGC 180
Qy 273 GACCCGAGCCCGGAGAGCGGAGCGCGCTCTCCCGCGCGCGCTCTGATGCGGGC 332
Db 181 GACCCGAGCCCGGAGAGCGGAGCGCGCTCTCCCGCGCGCGCTCTGATGCGGGC 240
Qy 333 CCCAGCTTCGGGCGCGCGGAGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 392
Db 241 CCCAGCTTCGGGCGCGCGGAGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
Qy 393 GCGGCGCGCGCGCGCTCCATGACAGCGCTTGAAGGGGTCACAGAGCGCGCGCG 452
Db 301 GCGGCGCGCGCGCGCTCCATGACAGCGCTTGAAGGGGTCACAGAGCGCGCGCG 360
Qy 453 CCGCGGAGCGCCCAATGTCTCTGACGTCACGTCGCAACGCTTTGTTCAGAGCA 512
Db 361 CCGCGGAGCGCCCAATGTCTCTGACGTCGCAACGCTTTGTTCAGAGCA 420
Qy 513 TGAATCAGGAGCTGAGTTTGTTCATCATCATCATCATCATCATCATCATCATCAT 572
Db 421 TGAATCAGGAGCTGAGTTTGTTCATCATCATCATCATCATCATCATCATCATCAT 480
Qy 573 TGGTGTGTGTATACGTCGCTGTCGCACTCAAGGCTGTGCAAGGCTCTTATCA 632
Db 481 TGGTGTGTGTATACGTCGCTGTCGCACTCAAGGCTGTGCAAGGCTCTTATCA 540
Qy 633 GCCGCAAGCGAGGCGGAGAGAGAGATGCTCTCTCAAGAGATGCTGTGCG 692
Db 541 GCCGCAAGCGAGGCGGAGAGAGAGATGCTCTCTCAAGAGATGCTGTGCG 600
Qy 693 CTTGAGAGAGCAGTGTCAAGGCAAGGATCCAGAGCGGAGGCTTAAGCCCGCTC 752
Db 601 CTTGAGAGAGCAGTGTCAAGGCAAGGATCCAGAGCGGAGGCTTAAGCCCGCTC 660
Qy 753 GGGCCACCGACCGCTGGCGGCTGCGGCTTGGCGGAGCGGAGCGCTTCCAGCGCTTC 812
Db 661 GGGCCACCGACCGCTGGCGGCTGCGGCTTGGCGGAGCGGAGCGCTTCCAGCGCTTC 720
Qy 813 AGCCCACTATCCCTATCTGAGAGAGATGCACTTGCACCCAGCATCTGCTGTAG 872
Db 721 AGCCCACTATCCCTATCTGAGAGAGATGCACTTGCACCCAGCATCTGCTGTAG 780
Qy 873 AGCGGAGAGAGCGCCCACTTACCAAGGCGCTGACCTTCAAGCTTGGAGCCCGAGC 932
Db 781 AGCGGAGAGAGCGCCCACTTACCAAGGCGCTGACCTTCAAGCTTGGAGCCCGAGC 840
Qy 933 AGCAGCTGGAATCAACCGGAGTGGTGGCGGAGCGCGCGCGCGCGCGCGCGCG 992
Db 841 AGCAGCTGGAATCAACCGGAGTGGTGGCGGAGCGCGCGCGCGCGCGCGCGCGCG 900
Qy 993 GTACCTGATGATGATGTCAGGCTGGGCGGCGCTGCGCGCGCGCGCGCGCGCGCA 1052

QY 813 AGCCCACTATCCGTAACCTGAGACGAGATGCACTTGCCACCCACCATTCTGGTGCAG 872
 DB 721 AGCCCACTATCCGTAACCTGAGACGAGATGCACTTGCCACCCACCATTCTGGTGCAG 780
 QY 873 ACGGGAG 932
 DB 781 ACGGGAG 840
 QY 933 AGCAGCTGGAATGAACTGGAAGTGTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 992
 DB 841 AGCAGCTGGAATGAACTGGAAGTGTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
 QY 993 GTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1052
 DB 901 GTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
 QY 1053 TCAGCGCCAGCTGCTACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1112
 DB 961 TCAGCGCCAGCTGCTACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
 QY 1113 AGGTGATGCGCTACTACCCGGGCTCTCTCTTCAGACACAGACAGAGAGAGAGAGAGAG 1172
 DB 1021 AGGTGATGCGCTACTACCCGGGCTCTCTCTTCAGACACAGAGAGAGAGAGAGAGAGAG 1080
 QY 1173 CCTTGTCTGAG 1232
 DB 1081 CCTTGTCTGAG 1140
 QY 1233 TCTGAGAGCAAG 1292
 DB 1141 TCTGAGAGCAAG 1200
 QY 1293 GGGCTGGGGCTGCTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1321
 DB 1201 GGGCTGGGGCTGCTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1229

RESULT 6
 ADP65729
 ID ADP65729 standard; DNA; 4839 BP.

AC ADP65729;
 XX 12-AUG-2004 (first entry)
 DE Human transmembrane, prostate androgen induced RNA (TMEMPA1), DNA.
 KW autoimmune disease; arthritis; gene expression analysis; antirheumatic;
 KW rheumatoid arthritis; collagen-induced; immunosuppressive; dermatological;
 KW antiarthritic; osteopathic; antigout; antiinflammatory; fibrositis;
 KW immunomodulatory; lupus; ankylosing spondylitis; fibrositis;
 KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
 KW immune; ds; human.
 XX Homo sapiens.
 OS
 PN WO2003072827-A1.
 XX 04-SEP-2003.
 XX 31-OCT-2002; 2002MO-US035433.
 XX 31-OCT-2001; 2001US-0336220P.
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 XX Hirsch R, Thornton SL;
 DR WPI; 2003-712740/67.
 DR GENBANK; NM_020182.
 PT Diagnosing and analyzing autoimmune disease using gene expression
 profiles and microarray technology, useful for diagnosing and treating

PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
 PT gout.
 XX Disclosure, Page; 56pp; English.
 PS
 XX The invention relates to a novel method for diagnosing and analysing
 CC autoimmune disease or arthritides. The method comprises obtaining a
 CC patient sample containing mRNA, analysing gene expression using the mRNA
 CC that results in a gene expression signature of the mRNA, and using that
 CC gene expression signature to diagnose or analyse the autoimmune disease
 CC or arthritides in the patient, where gene expression of at least 60% of
 CC the genes correlates with that of the gene signature. The invention
 CC further comprises: a treatment of rheumatoid arthritis; identification
 CC of genes for targeting in the treatment of rheumatoid arthritis in a mammal
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
 CC analyses of autoimmune disease or rheumatoid arthritis; screening the
 CC efficacy of a candidate drug in vitro for the treatment of collagen-
 CC induced arthritis; and reducing the symptoms associated with collagen-
 CC induced arthritis. The compositions of the invention have the following
 CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
 CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
 CC methods and compositions of the present invention are useful for
 CC diagnosing and treating autoimmune disease or arthritides, such as
 CC fibromyalgia, osteoarthritis, lupus, ankylosing spondylitis, fibrositis,
 CC rheumatoid arthritis, gout, juvenile rheumatoid arthritis, and an
 CC immune disease caused by an infectious agent. This polynucleotide
 CC represents a DNA sequence relating to the genes used in the analysis and
 CC treatment of autoimmune diseases or arthritides. Note: This sequence is
 CC not shown in the specification. It has been supplied in an electronic
 CC format from WIPO.
 XX
 SQ Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other:
 Query Match 93.0%; Score 1229; DB 11; Length 4839;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 93 GGAAAGCTAAGCGGAG 152
 DB 1 GGAAAGCTAAGCGGAG 60
 QY 153 TTCCGAG 212
 DB 61 TTCCGAG 120
 QY 213 GGGGAG 272
 DB 121 GGGGAG 180
 QY 273 GAGCCGAG 332
 DB 181 GAGCCGAG 240
 QY 333 CCCAGCTCCGGGAG 392
 DB 241 CCCAGCTCCGGGAG 300
 QY 393 GCGCGAG 452
 DB 301 GCGCGAG 360
 QY 453 CCGCGGAG 512
 DB 361 CCGCGGAG 420
 QY 513 TGAGATCAG 572
 DB 421 TGAGATCAG 480
 QY 573 TGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 632
 DB 481 TGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540

QY	573	TGAGGAGTGATCAACGGCTCGCTGACCACTCAACAACTGCTGCAAGGTCCTTATCA	632
Db	481	TGATGTGTGTATCACTGCTCTGCTGACCACTACAACTGTCTGCAAGGTCCTTATCA	540
QY	633	GCCGCGCACAGCCAGAGGCGGAGAGAGAGATGCCCCCTGTCTCTCAGAAAGATGCCCTGAGC	692
Db	541	GCCGCGCACAGCCAGAGGCGGAGAGAGAGATGCCCCCTGTCTCTCAGAAAGATGCCCTGAGC	600
QY	693	CCTTGGAGAGACACATGTCTCAGGCAACGGAAATCCCAAGACCCGCAAGTCTAAGCCCCGCTTC	752
Db	601	CCTTGGAGAGACACATGTCTCAGGCAACGGAAATCCCAAGACCCGCAAGTCTAAGCCCCGCTTC	660
QY	753	GGCCCAACCGACCGGCTGTGCGCGGCGCCCTTTCGCCACAGCGGAGGGCTTCCACCGCTTCC	812
Db	661	GGCCCAACCGACCGGCTGTGCGCGGCGCCCTTTCGCCACAGCGGAGGGCTTCCACCGCTTCC	720
QY	813	AGCCCAACCTATCCGTACTGTGACGACGAGATCGACTTGCACCCACATCTTGTGTGAG	872
Db	721	AGCCCAACCTATCCGTACTGTGACGACGAGATCGACTTGCACCCACATCTTGTGTGAG	780
QY	873	ACGGGAGAGAGACCCCAACCTTACAGGGGCCCCCTGCACCTCTCAAGTTTGGGAGCCCCGAGC	932
Db	781	ACGGGAGAGAGACCCCAACCTTACAGGGGCCCCCTGCACCTCTCAAGTTTGGGAGCCCCGAGC	840
QY	933	AGCAGCTGGAACCTGAACCGGGGAGTGTGTGTGCGCGACCCCCCAAGAAACATCTTTCGACA	992
Db	841	AGCAGCTGGAACCTGAACCGGGGAGTGTGTGTGCGCGACCCCCCAAGAAACATCTTTCGACA	900
QY	993	GTGACCTGATGGATGTAGTGCACAGGCTGTGGCGGCGCCCTGTGCCCCCGACAGTAACTTGGGCA	1052
Db	901	GTGACCTGATGGATGTAGTGCACAGGCTGTGGCGGCGCCCTGTGCCCCCGACAGTAACTTGGGCA	960
QY	1053	TCAGCGCCACGTGTCTTACGCGACGCGGCGGCGCATGTGAAGGGGCGCGCGCCACCTTACAGCG	1112
Db	961	TCAGCGCGACGTGTCTTACGCGACGCGGCGGCGCATGTGAAGGGGCGCGCGCCACCTTACAGCG	1020
QY	1113	AGGTCAATGGGCACTAACCCGGGGGTCTCTCTTCAACACACAGAGAGAGCATGTGGGCGCGCCT	1172
Db	1021	AGGTCAATGGGCACTAACCCGGGGGTCTCTCTTCAACACACAGAGAGAGCATGTGGGCGCGCCT	1080
QY	1173	CCTTGCTGAGGGGAGACCGGCTCCACACACACACATCGCGCCCCCTTAGAGAGCGAGCA	1232
Db	1081	CCTTGCTGAGGGGAGACCGGCTCCACACACACACATCGCGCCCCCTTAGAGAGCGAGCA	1140
QY	1233	TCTGGAGCAAAAGAGAGATAAACAGAAAGACACCTTCTTAGGGGTCCCGAGGGGGGCTC	1292
Db	1141	TCTGGAGCAAAAGAGAGATAAACAGAAAGACACCTTCTTAGGGGTCCCGAGGGGGGCTC	1200
QY	1293	GGGCTGGGGCTGCCATAGGTGAATAAGGCGAG	1321
Db	1201	GGGCTGGGGCTGCCATAGGTGAATAAGGCGAG	1229

RESULT	8
ADRe5875	
ID	ADRe5875 standard; DNA; 4839 BP.
XX	
AC	ADRe5875;
DT	02-DEC-2004 (first entry)
XX	
DE	Human prostatic carcinoma derived DNA SEQ ID 71 #1
XX	
KW	human; cytostatic; diagnosis; prostatic cancer; differential expression analysis; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO2004076614-A2.
XX	
PD	10-SEP-2004.
XX	
PF	22-FEB-2004; 2004WO-DE000433.

XX 27-FEB-2003; 2003DE-01009985.
PR 14-MAY-2003; 2003DE-01022134.
XX
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
XX (PILA/) PILARSKY C.
PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarczyk C, Specht T;
PI Schmitt A, Bechmann G, Bruemendorf T, Kinnemann H, Roepcke S;
PI Xinzhong L, Steub E;
XX
XX WPI; 2004-653386/63.
DR
XX
XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,
PT useful for diagnosis, treatment and in screening for specific binding
PT agents.
XX
XX
XX Claim 1; Page 277; 1607pp; German.

This invention describes novel cytosratic polynucleotide and polypeptide sequences which can be used in a method for diagnosing prostatic cancer or the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or over expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection substances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonucleotides, short-interfering RNA or ribozymes; an organic molecule of molecular weight below 5000, preferably 300, that binds to the polypeptide; an aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the polypeptide, preferably humanised or human; an anti-idiotypic, non-human (monoclonal) antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or radioisotope. The polynucleotides are identified in human prostatic cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over)expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of tissue, isolated from prostatic cancer patients, or subjects at risk, were incubated sequentially with anti-human CD4 murine monoclonal antibodies; biotinylated second antibody; streptavidin-conjugated horseradish peroxidase and then diaminobenzidine as colour former (brown). The samples were counterstained with hemalum (blue). Malignant cells stained strongly but non-malignant cells only weakly. In 15 of 63 samples of adenocarcinoma, membrane and cytoplasmic staining was very strong, and lymph node metastases were also stained. ADR65805-ADR66954 represent the polynucleotide and polypeptide sequences used in the method of the invention.

Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;

Query Match	93.0%	Score 1229	DB 13	Length 4839
Best Local Similarity	100.0%	Pred. No. 0		
Matches 1259	0	Mismatches	0	Indels 0
				Gaps 0

QY 93 GGAAGCTAGAGGCGAGAGGCTCAGGCCCCGGGCGGCAAGCGCGCCCCGCTGCAGGCCATT 152

Db 1 GGAAGCTAGAGGCGAGAGGCTCAGGCCCCGGGCGGCAAGCGCGCCCCGCTGCAGGCCATT 60

QY 153 TTCCGAGATGCCACCCGCGGGGCACTGCCGACGCGCCCCGGGGCTGCCGAGGGAGGCCGGGG 212

Db 61 TTCCGAGATGCCACCCGCGGGCACTGCCGACGCGCCCCGGGGCTGCCGAGGGAGGCCGGGG 120

QY 213 GGGCGCACGAGAGCGCGGTCCTCCGCGCATCTAGACCCCGCGGCGTCCCGGGACCTTGCGGGC 272

Db 121 GGGCGCACGAGAGCGCGGTCCTCCGCGCATCTAGACCCCGCGGCGTCCCGGGACCTTGCGGGC 180

QY 273 GACCCGAGCCGCGGCGAGCGCGGGCGCGCTTCCCGCGCGCGGCTCTGATCGGGGC 332

Db 181 GACCCGAGCCGCGGCGAGCCGCGGCGGCTCCCGCGCGCGGCTCCTCGATGCGGCGG 240
 Qy 333 CCCAGCTCCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 392
 Db 241 CCCAGCTCCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
 Qy 333 GCGCGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 452
 Db 301 GCGCGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
 Qy 453 CGCGCGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 512
 Db 361 CGCGCGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
 Qy 513 TGGAGATCA CGAGAGCTGAGATTGTTGATCATCATCATCATCATCATCATCATCATCATCA 572
 Db 421 TGGAGATCA CGAGAGCTGAGATTGTTGATCATCATCATCATCATCATCATCATCATCATCA 480
 Qy 573 TGGAGATCA CGAGAGCTGAGATTGTTGATCATCATCATCATCATCATCATCATCATCATCA 632
 Db 481 TGGAGATCA CGAGAGCTGAGATTGTTGATCATCATCATCATCATCATCATCATCATCATCA 540
 Qy 633 GCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 692
 Db 541 GCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
 Qy 693 CCGCGGAGAGCA GAGTGTGAGGCGAAGGATCCAGAGCGGAGGCTTACGCGCGCGCTG 752
 Db 601 CCGCGGAGAGCA GAGTGTGAGGCGAAGGATCCAGAGCGGAGGCTTACGCGCGCGCTG 660
 Qy 753 GCGCGGAGAGCA GAGTGTGAGGCGAAGGATCCAGAGCGGAGGCTTACGCGCGCGCTG 812
 Db 661 GCGCGGAGAGCA GAGTGTGAGGCGAAGGATCCAGAGCGGAGGCTTACGCGCGCGCTG 720
 Qy 813 AGCCGACCTATCGATACCTGACGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 872
 Db 721 AGCCGACCTATCGATACCTGACGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 780
 Qy 873 AGCGGAGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 932
 Db 781 AGCGGAGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840
 Qy 933 AGCGGAGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 992
 Db 841 AGCGGAGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 900
 Qy 993 AGCGGAGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1052
 Db 901 AGCGGAGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 960
 Qy 1053 AGCGGAGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1112
 Db 961 AGCGGAGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1020
 Qy 1113 AGCGGAGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1172
 Db 1021 AGCGGAGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1080
 Qy 1173 AGCGGAGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1232
 Db 1081 AGCGGAGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1140
 Qy 1233 AGCGGAGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1292
 Db 1141 AGCGGAGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1200
 Qy 1293 AGCGGAGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1321
 Db 1201 AGCGGAGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1229

RESULT 9
 ADR66778

ID ADR66778 standard; DNA; 4839 BP.
 AC ADR66778;
 DT 02-DEC-2004 (first entry)
 XX
 DE Human prostatic carcinoma derived DNA SEQ ID 71 #4.
 XX human; cyrostatic; diagnosis; prostatic cancer;
 KM differential expression analysis; ds.
 XX Homo sapiens.
 OS
 PN MO2004076614-A2.
 PD 10-SEP-2004.
 PF 22-FEB-2004; 2004MO-DE000433.
 PR 27-FEB-2003; 2003DE-01009985.
 PR 14-MAY-2003; 2003DE-01022134.
 XX
 PA (HINZ/) HINZMANN B.
 PA (DAHL/) DAHL E.
 PA (ROSE/) ROSENTHAL A.
 PA (HERM/) HERMANN K.
 PA (PILAU/) PILARSKY C.
 PI Hinmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;
 PI Schmitt A, Beckmann G, Bruemendorf T, Kinemann H, Roepcke S;
 PI Xinhong L, Staub E;
 DR WPI; 2004-653386/63.
 PT New nucleic acids, and encoded proteins, from prostatic cancer tissue,
 PT useful for diagnosis, treatment and in screening for specific binding
 PT agents.
 PS
 PS Claim 1; Page 1447; 1607pp; German.
 XX
 CC This invention describes novel cyrostatic polynucleotide and polypeptide
 CC sequences which can be used in a method for diagnosing prostatic cancer
 CC or the risk of developing prostatic cancer. Diagnosis is based on
 CC determining over transcription or over expression of the sequences in
 CC prostatic tissue. Screening for inhibitors of the sequences or detection
 CC substances involves a binding assay, any compounds that bind are
 CC selected, optionally after deconvolution of mixtures. Detection of a
 CC predetermined minimum level of the reporter indicates the presence of
 CC tumor cells. Inhibitors can be chosen from antisense oligonucleotides,
 CC short-interfering RNA or ribozymes; an organic molecule of molecular
 CC weight below 5000, preferably 300, that binds to the polypeptide; an
 CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
 CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human
 CC (monoclonal) antibody directed against Ab or any of the above derivatised
 CC with a reporter group, cell toxin, immunostimulatory molecules and/or
 CC radioisotope. The polynucleotides are identified in human prostatic
 CC cancer by differential expression analysis, using DNA microarrays,
 CC between normal and tumorous tissues, with (over)expression being detected
 CC by quantitative PCR. Analysis of prostatic cancer samples showed that
 CC CD24 was upregulated in many of them. Sections of tissue, isolated from
 CC prostatic cancer patients, or subjects at risk, were incubated
 CC sequentially with anti-human CD4 murine monoclonal antibodies;
 CC biotinylated second antibody; streptavidin-conjugated horseradish
 CC peroxidase and then diaminobenzidine as colour former (brown). The
 CC samples were counterstained with hemalum (blue). Malignant cells stained
 CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
 CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
 CC lymph node metastases were also stained. ADR6505-ADR6694 represent the
 CC polynucleotide and polypeptide sequences used in the method of the
 CC invention.
 SQ Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;

Query Match 93.0%; Score 1229; DB 13; Length 4839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 GGAAGCTAGAGGCGAGAGCTCAGCCCGGCGGAGCGGCGCCCGCTGCGAGCCCAT 152
Db 1 GGAAGCTAGAGGCGAGAGCTCAGCCCGGCGGAGCGGCGCCCGCTGCGAGCCCAT 60

Qy 153 TTCCGAGCGCCACCCCGGCGGCACTGCGGACGCCCCCGGGGCTGCCGAGGGAGCGG 212
Db 61 TTCCGAGCGCCACCCCGGCGGCACTGCGGACGCCCCCGGGGCTGCCGAGGGAGCGG 120

Qy 213 GGGGCGACCGGAGCGCGGCTCCCGGCACTGAGCCCCCGGGGCGCCCGGGAATTGGCGGC 272
Db 121 GGGGCGACCGGAGCGCGGCTCCCGGCACTGAGCCCCCGGGGCGCCCGGGAATTGGCGGC 180

Qy 273 GACCCGAGCCCGGCGAGCGGGGCGGCGCTCCCGGCGGCGGCTCTGCGATGCGGGGC 332
Db 181 GACCCGAGCCCGGCGAGCGGGGCGGCGCTCCCGGCGGCGGCTCTGCGATGCGGGGC 240

Qy 333 CCGAGCTCCGGGCGCGGCGCGGAGCGCCCCCGGCGCGCCCGAGCCCCCGCGCGC 392
Db 241 CCGAGCTCCGGGCGCGGCGCGGAGCGCCCCCGGCGCGCCCGAGCCCCCGCGCGC 300

Qy 393 GCGGCGCGCGCGCGCGCTCCAGTCAACCGCTTGAAGGGGCTCAACAGCAACCGCGCGCG 452
Db 301 GCGGCGCGCGCGCGCGCTCCAGTCAACCGCTTGAAGGGGCTCAACAGCAACCGCGCGCG 360

Qy 453 CCGCGGCGAGCCCAATGCTCTCTGCGAGCTGCAATGCAACGCTCTTGTTCAGAGCA 512
Db 361 CCGCGGCGAGCCCAATGCTCTCTGCGAGCTGCAATGCAACGCTCTTGTTCAGAGCA 420

Qy 513 TGGAGATCAACGAGCTGAGATTGTTCAATCATATCATGTGGTGTGATGATGATGA 572
Db 421 TGGAGATCAACGAGCTGAGATTGTTGTTCATCATCATGTGGTGTGATGATGATGA 480

Qy 573 TGGTGTGGTGTATCAAGTGCCTGCTGAGCACTAACAGTGTCTGACAGGCTCTTCATCA 632
Db 481 TGGTGTGGTGTATCAAGTGCCTGCTGAGCACTAACAGTGTCTGACAGGCTCTTCATCA 540

Qy 633 GCGGCGAGCGCGGCGGCGAGAGAGAGATGCTGCTCTCAGAGAGATGCTGTGGC 692
Db 541 GCGGCGAGCGCGGCGGCGAGAGAGAGATGCTGCTCTCAGAGAGATGCTGTGGC 600

Qy 693 CCTCGAGAGCACTGCTGAGCAACGAGATCCAGAGCGCGAGGCTTACGCCCGCTC 752
Db 601 CCTCGAGAGCACTGCTGAGCAACGAGATCCAGAGCGCGAGGCTTACGCCCGCTC 660

Qy 753 GGGCCACCGAGCGCGGCGGCTGCGGCGCTTCCGCGAGCGGAGGCTTCCACGCGCTCC 812
Db 661 GGGCCACCGAGCGCGGCGGCTGCGGCGCTTCCGCGAGCGGAGGCTTCCACGCGCTCC 720

Qy 813 AGCCCACTATCCGTAACCTGAGCAACGAGATGAGCTGCAACCCACATCTTGCTGTGAG 872
Db 721 AGCCCACTATCCGTAACCTGAGCAACGAGATGAGCTGCAACCCACATCTTGCTGTGAG 780

Qy 873 ACGGAGAGAGGCGCCCACTTCAACAGAGGCGCTTGCACCTTCCAGGTTGGAGAGCCCGAGC 932
Db 781 ACGGAGAGAGGCGCCCACTTCAACAGAGGCGCTTGCACCTTCCAGGTTGGAGAGCCCGAGC 840

Qy 933 AGCAGCTGGAATGAAACCGGAGTGGGAGCGGCAACCCCAAGAGAGAGCAATCTTGCACA 992
Db 841 AGCAGCTGGAATGAAACCGGAGTGGGAGCGGCAACCCCAAGAGAGAGCAATCTTGCACA 900

Qy 993 GTGACCTGATGATAGTGCAGGCTTGGGCGGCGCTTCCCGCCAGCAAGTAACTCGGCA 1052
Db 901 GTGACCTGATGATAGTGCAGGCTTGGGCGGCGCTTCCCGCCAGCAAGTAACTCGGCA 960

Qy 1053 TCAGGCGCACTGCTTACGCGAGCGGCGGCGGCAATGAGAGGGCGCGCGCCACCTTACAGCG 1112
Db 961 TCAGGCGCACTGCTTACGCGAGCGGCGGCGGCAATGAGAGGGCGCGCGCCACCTTACAGCG 1020

Qy 1113 AGGTATCGGCGCACTAACCGGGGCTCTCTTCCAGAGCAACAGAGAGTGGGCGCGCT 1172

Db 1021 AGGTATCGGCGCACTAACCGGGGCTCTCTTCCAGAGCAACAGAGAGTGGGCGCGCT 1080

Qy 1173 CTTTGTGAGAGGAGACCCGGCTCCACACACACATCTGGGCGCCCTTGAAGAGCGAGCCA 1232

Db 1081 CTTTGTGAGAGGAGACCCGGCTCCACACACATCTGGGCGCCCTTGAAGAGCGAGCCA 1140

Qy 1233 TCTGAGCAAGAGAGATTAACAGAAAGGACACCCCTCTAGAGGTCCCGAGGGGGCC 1292

Db 1141 TCTGAGCAAGAGAGATTAACAGAAAGGACACCCCTCTTGAAGGTCCCGAGGGGGCC 1200

Qy 1293 GGGCTGGGCTGGCTAGTGAAGAGGAG 1321

Db 1201 GGGCTGGGCTGGCTAGTGAAGAGGAG 1229

RESULT 10
ADU06063
ID ADU06063 standard; DNA; 4839 BP.

AC ADU06063;
XX
XX
XX 27-JAN-2005 (first entry)
XX
XX
XX Novel bronchial cancer-associated human gene SegID285.
XX
XX bronchial cancer; cytostatic; tumour-associated protein;
XX cancer detection; metastasis; tumour; gene; ds; human.
XX Homo sapiens.
XX DE10316701-A1.
XX
XX 04-NOV-2004.
XX
XX 09-APR-2003; 2003DE-01016701.
XX
XX 09-APR-2003; 2003DE-01016701.
XX
XX 09-APR-2003; 2003DE-01016701.
XX
XX (HINZ/) HINZMANN B.
XX (HERM/) HERMANN K.
XX (CAST/) HEIDEN CASTANOS-VELEZ E.
XX
XX Mennertich D, Bruemendorf T, Heiden E, Hermann K, Kimmernann H;
XX Li X, Roepcke S, Staub E, Hinzmann B, Rosenthal A, Pilarsky C;
XX WPI; 2004-786403/78.
XX P-PSDB; ADU06550.
XX
XX New nucleic acid, and derived proteins, useful for diagnosis of bronchial
XX cancer and in screening for therapeutic and diagnostic agents.
XX
XX Claim 1; SEQ ID NO 285; 1381bp; German.
XX
XX This invention relates to a novel isolated nucleic acid associated with
XX bronchial cancer comprising 489 defined sequences given in the
XX specification. The invention may be useful for the production of
XX compounds with a cytostatic activity through the inhibition of expression
XX or activity of tumour-associated proteins. The novel DNA sequences and
XX the proteins/peptides encoded by them are used for detecting bronchial
XX cancer or determining the risk of developing it and to screen for
XX specific binding partners of the DNA or protein sequences, where the
XX binding partners are potentially useful as agents for treating or
XX diagnosing bronchial cancer. The DNA or protein sequences can also be
XX used for prognosis, detection of metastases and for secondary treatment
XX (of tumours that have been stabilised or are no longer detectable).
XX Detecting abnormal expression of the DNA sequences provides early
XX diagnosis of bronchial cancers. The present sequence is that of a novel
XX bronchial cancer-associated human gene sequence of the invention.
XX
XX Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;
XX

Query Match 93.0%; Score 1229; DB 13; Length 4839;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

93 GGAAGCTAGCGGAGAGGCTCAGGCTCCGCGGAGCGCGGCGCGCTGCGCAGCCATT 152
Db 1 GGAAGCTAGCGGAGAGGCTCAGGCTCCGCGGAGCGCGGCGCGCTGCGCAGCCATT 60

153 TTCCGAGCGCACTCCGCGGAGCTGCGCACTCCGCGGAGCTGCGGAGGAGGCGCGG 212
Db 61 TTCCGAGCGCACTCCGCGGAGCTGCGCACTCCGCGGAGCTGCGGAGGAGGCGCGG 120

213 GGGCGCAGCGGAGCGGCTCCGCGGAGCTGCGGAGCGCGGAGGAGGAGGAGGAGG 272
Db 121 GGGCGCAGCGGAGCGGCTCCGCGGAGCTGCGGAGCGCGGAGGAGGAGGAGGAGG 180

273 GACCCGAGCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 332
Db 181 GACCCGAGCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 240

333 CCCAGCTCCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 392
Db 241 CCCAGCTCCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 300

393 GCGCGCGCGCGCGCGCGCTCCAGCACTCCGCGGAGCGGAGCGGAGCGGAGCGG 452
Db 301 GCGCGCGCGCGCGCGCTCCAGCACTCCGCGGAGCGGAGCGGAGCGGAGCGGAG 360

453 CCGCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 512
Db 361 CCGCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 420

513 TGGAGATCAAGGAGCTGAGGTTGTTGATGATCATCATGCTGCTGATGATGATG 572
Db 421 TGGAGATCAAGGAGCTGAGGTTGTTGATGATCATCATGCTGCTGATGATGATG 480

573 TGGTGTGTGTATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 632
Db 481 TGGTGTGTGTATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540

633 GCGCGCAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 692
Db 541 GCGCGCAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 600

693 CCTCGAGAGCAGAGTGTGAGGCAACGAAATCCAGAGCGGAGCTTACGCGCGCT 752
Db 601 CCTCGAGAGCAGAGTGTGAGGCAACGAAATCCAGAGCGGAGCTTACGCGCGCT 660

753 GCGCGCAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 812
Db 661 GCGCGCAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 720

813 AGCCCACTATCCGATCTGAGCAGCAGAGATGACCTGCGCAGCCACATCTGCTG 872
Db 721 AGCCCACTATCCGATCTGAGCAGCAGAGATGACCTGCGCAGCCACATCTGCTG 780

873 AGCGGAGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGG 932
Db 781 AGCGGAGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGG 840

933 AGCAGCTGGAATCTGAAACCGGAGTGTGCTGCGGAGCGGAGCGGAGCGGAG 992
Db 841 AGCAGCTGGAATCTGAAACCGGAGTGTGCTGCGGAGCGGAGCGGAGCGGAG 900

993 GTGACCTGATGATGATGCTGCGGAGCTGCGGAGCGGAGCGGAGCGGAGCGG 1052
Db 901 GTGACCTGATGATGATGCTGCGGAGCTGCGGAGCGGAGCGGAGCGGAGCGG 960

1053 TTAGCGCCACGTGCTTACGCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 1112
Db 961 TTAGCGCCACGTGCTTACGCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 1020

1113 AGGTATGTGGCGCTACCGCGGCTCTCTTCCAGACAGAGAGCACTGAGCGCGCT 1172

Db 1021 AGGTATGTGGCGCTACCGCGGCTCTCTTCCAGACAGAGAGAGAGGAGCGGCT 1080
Gy 1173 CCTTGTGAGGAGGAGCGGAGCTCCAGCAGACAGATCGGCGGCTTGAAGCGCAGCCA 1232
Db 1081 CCTTGTGAGGAGGAGCGGAGCTCCAGCAGACAGATCGGCGGCTTGAAGCGCAGCCA 1140

Gy 1233 TCTGAGCAAAAGAGAGATTAACAGAAAGACACCTCTTGAAGGTCCCGAGGAGGAG 1292
Db 1141 TCTGAGCAAAAGAGAGATTAACAGAAAGACACCTCTTGAAGGTCCCGAGGAGGAG 1200

Gy 1293 GGGCTGAGGAGCTGCTGAGGTGAAAAGCAG 1321
Db 1201 GGGCTGAGGAGCTGCTGAGGTGAAAAGCAG 1229

RESULT 11
ADM43368
ID ADM43368 standard; DNA; 4839 BP.
XX
AC ADM43368;
XX
DT 24-MAR-2005 (first entry)
XX
DE Prostate cancer related gene, SEQ ID 166.
XX
KM Cytostatic; Gene Therapy; Prostate tumor; prostatic cancer; diagnosis;
XX ds; gene.
XX Homo sapiens.
XX OS
XX PN MO2004113571-A2.
XX
PD 29-DEC-2004.
XX
PP 25-JUN-2004; 2004WO-IB002394.
XX
PR 26-JUN-2003; 2003US-0482595P.
XX
PA (EXON-) EXONHIT THERAPEUTICS SA.
XX
PI Einstein R, McGowan KM, Pando MP;
XX
DR WPI, 2005-057996/06.
XX
XX New isolated nucleic acid sequence that is expressed by human prostate
PT cancer cells, useful as target for treating, preventing and/or diagnosing
PT cancers, particularly prostate cancer.
XX
PS Claim 1; SEQ ID NO 166; 198bp; English.
XX
CC The present invention relates to novel nucleic acid sequences that are
CC expressed by human prostate cancer cells. The nucleic acid sequences or
CC the encoded proteins are useful as targets for treating, preventing
CC and/or diagnosing cancers, particularly prostate cancer. The present
CC sequence is one such nucleic acid of the invention.
XX
SQ Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;

Query Match 93.0%; Score 1229; DB 14; Length 4839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

93 GGAAGCTAGCGGAGAGGCTCAGGCTCCGCGGAGCGCGGCGCGCTGCGCAGCCATT 152
Db 1 GGAAGCTAGCGGAGAGGCTCAGGCTCCGCGGAGCGCGGCGCGCTGCGCAGCCATT 60

153 TTCCGAGCGCACTCCGCGGAGCTGCGCACTCCGCGGAGCTGCGGAGGAGGCGCGG 212
Db 61 TTCCGAGCGCACTCCGCGGAGCTGCGCACTCCGCGGAGCTGCGGAGGAGGCGCGG 120

213 GGGCGCAGCGGAGCGGCTCCGCGGAGCTGCGGAGCGCGGAGGAGGAGGAGGAGG 272
Db 121 GGGCGCAGCGGAGCGGCTCCGCGGAGCTGCGGAGCGCGGAGGAGGAGGAGGAGG 180

DB 280 GCACAGTGTCAAGGCAACGGAATCCAGAGCCGAGAGTCTAAGCCCCCGCTGGGCCACCG 339
QY 762 ACCGCTGAGCGGTGCGCCCTTCCGACAGCGGAGCGCTTCCACCGCTTCCAGCCCACT 821
DB 340 ACCGCTGAGCGGTGCGCCCTTCCGACAGCGGAGCGCTTCCACCGCTTCCAGCCCACT 399
QY 822 ATCCGTACTCTGAGACGAGATCCGACCTGACCCACCATCTCGCTGTCACAGCGGAGG 881
DB 400 ATCCGTACTCTGAGACGAGATCCGACCTGACCCACCATCTCGCTGTCACAGCGGAGG 459
QY 882 AGCCCCCACTTACAGGAGCGCCCTGACCTTCCAGCTTCCGAGACCCGAGAGACAGCTGG 941
DB 460 AGCCCCCACTTACAGGAGCGCCCTGACCTTCCAGCTTCCGAGACCCGAGAGACAGCTGG 519
QY 942 AACTGAACCGGAGTGTGGTGGCGACCCGCCAACAAGAACCATCTTCCAGAGTGAAGCTGA 1001
DB 520 AACTGAACCGGAGTGTGGTGGCGACCCGCCAACAAGAACCATCTTCCAGAGTGAAGCTGA 579
QY 1002 TGGATAGTGCAGAGGTGGGCGGCGCCCTGCCCCCAGAGTAATCTGGGCGATCCAGCGGCA 1061
DB 580 TGGATAGTGCAGAGGTGGGCGGCGCCCTGCCCCCAGAGTAATCTGGGCGATCCAGCGGCA 639
QY 1062 CGTGTACGAGCGAGCGGCGGCGCATGAGAGGCGCGCCGCCCACTACAGCGAGTCAATCG 1121
DB 640 CCGTGTACGAGCGAGCGGCGGCGCATGAGAGGCGCGCCGCCCACTACAGCGAGTCAATCG 699
QY 1122 GCCACTACCGGAGGTCTCTCTTCCAGACACAGCAGAGAGAGTGGGCGCTCTTCTGGTGG 1181
DB 700 GCCACTACCGGAGGTCTCTCTTCCAGACACAGCAGAGAGAGTGGGCGCTCTTCTGGTGG 759
QY 1182 AGGGAGCCCGGTGCACACACACATCGGCGCCCTGAGAGGCGCACCATCTGGAGCA 1241
DB 760 AGGGAGCCCGGTGCACACACACATCGGCGCCCTGAGAGGCGCACCATCTGGAGCA 819
QY 1242 AAGAGAGGATMAAGAAAGAGACACCTCTCTAGAGTCCCCAGGAGGCGCGGCTGGGCG 1301
DB 820 AAGAGAGGATMAAGAAAGAGACACCTCTCTAGAGTCCCCAGGAGGCGCGGCTGGGCG 879
QY 1302 CTGGCTAGTGAAGAGCGAG 1321
DB 880 CTGGCTAGTGAAGAGCGAG 899

RESULT 21
ADL83313
ID ADL83313 standard; cDNA; 4527 BP.
XX AC ADL83313;
XX 20-MAY-2004 (first entry)
DT Human androgen responsive prostate specific nucleic acid, ARP2.
XX Human; ss; gene; androgen responsive prostate specific; ARP2;
DE prostate cancer; prostate pathology; benign prostatic hyperplasia;
XX prostatic; prostatic neoplasm.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
XX CDS 96..854
FT /*tag= a
FT /product= "ARP2"
FT misc_feature 1128..4509
FT /*tag= b
FT /note= "Claimed in claim 10"

US2003166520-A1.
04-SEP-2003.
28-MAR-2001; 2001US-00821812.

XX 28-MAR-2001; 2001US-00821812.
PR (LINE/) LIN B.
XX LIn B;
XX WPI: 2003-898096/82.
DR P-PSDB: ADL83314.
XX New substantially pure androgen responsive prostate specific nucleic acid
PT molecules and polypeptides, useful for diagnosing, preventing and
PT treating prostate cancer or other prostatic pathologies, e.g.
PT prostatics.
XX
PS Claim 9; SEQ ID NO 2; 43pp; English.
XX
CC The invention relates to a substantially pure androgen responsive
CC prostate specific (ARP) nucleic acid molecule selected from ARP1-ARPs
CC (appearing as ADL83312, ADL83313, ADL83315, ADL83317 and ADL83319. Also
CC included are methods of diagnosing or predicting susceptibility to a
CC prostate neoplastic condition in an individual, methods for treating or
CC reducing the severity of a prostate neoplastic condition in an
CC individual, a substantially pure ARP3, ARP4 or ARP5 polypeptide (or their
CC fragments), encoded by the above ARP3, ARP4 or ARP5 nucleic acid molecule,
CC respectively) and a binding agent comprising a molecule that selectively
CC binds the above ARP3, ARP4 or ARP5 polypeptide. The nucleic acid
CC molecules and polypeptides are useful in diagnosing, preventing and
CC treating prostate cancer or other prostate pathologies such as benign
CC prostatic hyperplasia or prostatics. The nucleic acid molecules are used
CC as hybridisation probes in various diagnostic procedures. The present
CC sequence is the ARP2 cDNA.
SQ Sequence 4527 BP; 1089 A; 1149 C; 1175 G; 1113 T; 0 U; 1 Other;
Query Match 60.6%; Score 800; DB 11; Length 4527;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 800; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 522 CGAGCTGAGAGTTGTCACATCATCATCTGCTGCTGAGATGATGATGCTGGTGG 581
DB 100 CGAGCTGAGAGTTGTCACATCATCATCTGCTGCTGAGATGATGATGATGATGATG 159
QY 582 TGATCAGCTGCTGCTGAGCGACCTACAGAGCTGTGACGAGTCTCTCATCAGCGGAGCA 641
DB 160 TGATCAGCTGCTGCTGAGCGACCTACAGAGCTGTGACGAGTCTCTCATCAGCGGAGCA 219
QY 642 GCCAGGCGGAGAGAGAGATGCTCTGCTCTGAGAGATGCTGCTGCTGCTGCTGAGAG 701
DB 220 GCCAGGCGGAGAGAGAGATGCTCTGCTCTGAGAGATGCTGCTGCTGCTGCTGAGAG 279
QY 702 GCACAGTGTCAAGGAGAGATGCTCTGCTCTGAGAGATGCTGCTGCTGCTGCTGAGAG 761
DB 280 GCACAGTGTCAAGGAGAGATGCTCTGCTCTGAGAGATGCTGCTGCTGCTGCTGAGAG 339
QY 762 AGCGCTGAGCGGTGCGCCCTTCCGACAGCTTCCAGCTTCCAGCGGAGCACT 821
DB 340 AGCGCTGAGCGGTGCGCCCTTCCGACAGCTTCCAGCTTCCAGCGGAGCACT 399
QY 822 ATCCGTACTCTGAGACGAGATCCGACCTGACCCACCATCTCGCTGTCACAGCGGAGG 881
DB 400 ATCCGTACTCTGAGACGAGATCCGACCTGACCCACCATCTCGCTGTCACAGCGGAGG 459
QY 882 AGCCCCCACTTACAGGAGCGCCCTGACCTTCCAGCTTCCGAGACCCGAGAGACAGCTGG 941
DB 460 AGCCCCCACTTACAGGAGCGCCCTGACCTTCCAGCTTCCGAGACCCGAGAGACAGCTGG 519
QY 942 AACTGAACCGGAGTGTGGTGGCGACCCGCCAACAAGAACCATCTTCCAGAGTGAAGCTGA 1001
DB 520 AACTGAACCGGAGTGTGGTGGCGACCCGCCAACAAGAACCATCTTCCAGAGTGAAGCTGA 579
QY 1002 TGGATAGTGCAGAGGTGGGCGGCGCCCTGCCCCCAGAGTAATCTGGGCGATCCAGCGGCA 1061

PD 14-JUL-2005.
 XX 23-DEC-2004; 2004WO-DK000914.
 XX 27-DEC-2003; 2003DK-00001940.
 XX 24-JAN-2004; 2004DK-00000096.
 PR 07-APR-2004; 2004DK-00000586.
 PR 26-NOV-2004; 2004DK-00001843.
 XX (AROS-) AROS APPLIED BIOTECHNOLOGY APS.
 XX Ornhoft TF, Jensen JL, Krueffer W, Laiho P, Aaltonen LA;
 PI WPI; 2005-506661/51.
 XX Classifying the cancer in an individual having contracted cancer
 PT comprises determining the microsatellite status of the tumor.
 XX
 PS Claim 9; SEQ ID NO 127; 338bp; English.
 CC The invention relates to a method of classifying the cancer in an
 CC individual having contracted cancer, which comprises determining the
 CC microsatellite status of the tumor. The microsatellite status or the
 CC hereditary or sporadic nature of the cancer is determined by a method
 CC comprising: (a) obtaining a sample from the individual having contracted
 CC cancer; the sample comprising gene expression products, the presence
 CC and/or amount of which forms a pattern that is indicative of the
 CC microsatellite status or the hereditary or sporadic nature of the cancer;
 CC (b) determining the presence and/or amount of the gene expression
 CC products forming the pattern, and obtaining an indication of the
 CC microsatellite status or the hereditary or sporadic nature of the cancer
 CC in the individual based on step (b). At least one or two of the gene
 CC expression products forming a pattern used to determine the
 CC microsatellite status or the hereditary or sporadic nature of the cancer
 CC are selected individually from any of the 134 genes comprising 367-7850
 CC bp (AB222706 to AB22833), given in the specification. Also included are:
 CC a method for treating an individual; a method for reducing malignancy of
 CC a cell; a method for producing antibodies against an expression product
 CC of a cell from a biological tissue; pharmaceutical composition, for
 CC treating a classified cancer, comprising at least one antibody, at least
 CC one polypeptide, or at least one nucleic acid and/or probe; and an assay,
 CC for classification of cancer in an individual having contracted cancer,
 CC comprising at least one marker capable of determining the microsatellite
 CC status in a sample and at least one marker in a sample determining the
 CC prognostic marker, where the microsatellite status and the prognostic
 CC marker is determined simultaneously or sequentially. The method above is
 CC useful for producing an assay for classifying cancer in animal tissue.
 CC The peptide, gene, or probe is useful for preparing a pharmaceutical
 CC composition for the treatment of a cancer in animal tissue. The method is
 CC useful for classifying the cancer in an individual having contracted
 CC cancer, i.e. colon cancer, e.g. an adenocarcinoma, a carcinoma, a
 CC teratoma, a sarcoma, and/or a lymphoma. The present sequence represents a
 CC colon cancer-associated gene used in the method of the invention.
 XX
 SQ Sequence 4538 BP; 1090 A; 1151 C; 1179 G; 1118 T; 0 U; 0 Other;
 Query Match 60.6%; Score 800; DB 14; Length 4538;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 800; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 291 GCACAGTGTACAGGCAAGAAATCCAGAGCCGAGGCTCTACAGCCCGCTCGGCCACCG
 Qy 762 ACCGCTGCGCCCTGCGCCCTTGGCCAGGCGGAGCGCTTCACCGCTTCAGGCCACT
 Db 351 ACCGCTGCGCCCTGCGCCCTTGGCCAGGCGGAGCGCTTCACCGCTTCAGGCCACT
 Qy 822 ATCCGTACTGACAGCAGAGATGACCTGACACCCACCATCTGCTGTACAGCGGAGG
 Db 411 ATCCGTACTGACAGCAGAGATGACCTGACACCCACCATCTGCTGTACAGCGGAGG
 Qy 882 AGCCCCACCTTACAGAGGCGCCCTGACACCTTCCAGCTTCCGAGCCCGAGAGCAGCTGG
 Db 471 AGCCCCACCTTACAGAGGCGCCCTGACACCTTCCAGCTTCCGAGCCCGAGAGCAGCTGG
 Qy 942 AACTGAACCGGAGATCGGTGCGCGCCACCCCAACACAACTTTGACAGTACCTGA
 Db 531 AACTGAACCGGAGATCGGTGCGCGCCACCCCAACACAACTTTGACAGTACCTGA
 Qy 1002 TGATAGTGCAGGCTGGGGGCGCCCTGCGCCCGCCAGCAGTAACTCGGGCATCAGCCCA
 Db 591 TGATAGTGCAGGCTGGGGGCGCCCTGCGCCCGCCAGCAGTAACTCGGGCATCAGCCCA
 Qy 1062 CGTGTACGCGAGCGCGCGCGCATGAGAGGGGCGCCGACCTACAGCGAGGTCAATCG
 Db 651 CGTGTACGCGAGCGCGCGCGCATGAGAGGGGCGCCGACCTACAGCGAGGTCAATCG
 Qy 1122 GCCACTACCGCGGGTCTCTCTTCCAGACACAGCAGAGCAGTGGCGCCCTCTTGTCTGG
 Db 711 GCCACTACCGCGGGTCTCTCTTCCAGACACAGCAGAGCAGTGGCGCCCTCTTGTCTGG
 Qy 1182 AGGGAGCCCGGCTCCACACACACATGCGGCCCTTAGAGAGCGAGCCATCTGAGCA
 Db 771 AGGGAGCCCGGCTCCACACACACATGCGGCCCTTAGAGAGCGAGCCATCTGAGCA
 Qy 1242 AAGAGAGATTAACAGAAAGACACCTCTCTAGGGTCCCGAGGGGGCGCGGCTGAGG
 Db 831 AAGAGAGATTAACAGAAAGACACCTCTCTAGGGTCCCGAGGGGGCGCGGCTGAGG
 Qy 1302 CTGCGTAGTGAAGAGCAG 1321
 Db 891 CTGCGTAGTGAAGAGCAG 910
 Db
 RESULT 25
 AA157868
 ID AA157868 standard; cDNA; 1066 BP.
 XX
 AC AA157868;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polynucleotide SEQ ID NO 71.
 XX
 KW Human; noctropic; immunosuppressant; cyrostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; Chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia; ss.
 XX
 OS Homo sapiens.
 OS
 PN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000WO-US034263.
 XX
 PR 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-00488725.
 PR 25-APR-2000; 2000US-00552317.
 PR 20-JUN-2000; 2000US-00598042.

CC method of inhibiting the growth of a prostate cancer cell; (3) a method
 CC of modulating the expression of a gene in a prostate cancer cell, where
 CC transcription of the gene is regulated by an androgen receptor; (4) a
 CC method for diagnosing or prognosing prostate cancer; (5) a method of
 CC screening for compounds that specifically bind to (1); and (6) a method
 CC of evaluating the efficacy of a treatment in a patient with prostate
 CC cancer. (1) has cytostatic activity, and can be used in gene therapy. (1)
 CC polypeptides and polynucleotide can be used in reducing the expression of
 CC an androgen receptor in a prostate cancer cell, inhibiting the growth of
 CC a prostate cancer cell, modulating the expression of a gene in a prostate
 CC cancer cell, diagnosing or prognosing prostate cancer, evaluating the
 CC efficacy of a treatment in a patient with prostate cancer, treating
 CC hyperproliferative and hypoproliferative disorders or in gene therapy.

XX. Sequence 759 BP; 152 A; 269 C; 226 G; 112 T; 0 U; 0 Other;

Query Match 57.2%; Score 755; DB 10; Length 759;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 755; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 522 CGAGCTGAGTTTGTTCAGATCATCATCTGTGTGTATGATGTGTGTGTG 581
 DB 5 CGAGCTGAGTTTGTTCAGATCATCATCTGTGTGTATGATGTGTGTGTG 64
 QY 582 TGAATCAGTGTCTGTGACCACTAAGCTGTTCAGAGCTTTCATCAGCCGCA 641
 DB 65 TGAATCAGTGTCTGTGACCACTAAGCTGTTCAGAGCTTTCATCAGCCGCA 124
 QY 642 GCCAGGGGGGAGAGAGAGATGCGCTGTCTCAGAGAGATGCTGTGGCCCTCGAGA 701
 DB 125 GCCAGGGGGGAGAGAGAGATGCGCTGTCTCAGAGAGATGCTGTGGCCCTCGAGA 184
 QY 702 GCACAGTGTCAAGCAACGGAATCCAGAGCCGAGGTCTAGCCGCCCTCGAGCCCA 761
 DB 185 GCACAGTGTCAAGCAACGGAATCCAGAGCCGAGGTCTAGCCGCCCTCGAGCCCA 244
 QY 762 ACCGCTGTGCGCCCTTTCGCCAGCGGAGGCTTTCACCGCTTTCAGCCCACT 821
 DB 245 ACCGCTGTGCGCCCTTTCGCCAGCGGAGGCTTTCACCGCTTTCAGCCCACT 304
 QY 822 ATCCGACTGACGACGAGATGACCTTCCACCCACATCTGTGTGACAGCGGAG 881
 DB 305 ATCCGACTGACGACGAGATGACCTTCCACCCACATCTGTGTGACAGCGGAG 364
 QY 882 AGCCCCCACCCTTACAGAGGCGCCCTGACCTTCAGGTTGAGAGCCCGAGCAGCTG 941
 DB 365 AGCCCCCACCCTTACAGAGGCGCCCTGACCTTCAGGTTGAGAGCCCGAGCAGCTG 424
 QY 942 AACTGAACCGGAGTGTGCGCGCACCCCAAGAACATCTTTCAGACATGACCTGA 1001
 DB 425 AACTGAACCGGAGTGTGCGCGCACCCCAAGAACATCTTTCAGACATGACCTGA 484
 QY 1002 TGGATGTGTGCGGAGGCGGCGCCCTGACCCCGCCAGAGTAACTGCGGATCAGGCCA 1061
 DB 485 TGGATGTGTGCGGAGGCGGCGCCCTGACCCCGCCAGAGTAACTGCGGATCAGGCCA 544
 QY 1062 CGTGTACCGGACGCGGCGGCGCATGAGAGGCGCGCCCACTTACAGCGAGTATCG 1121
 DB 545 CGTGTACCGGACGCGGCGGCGCATGAGAGGCGCGCCCACTTACAGCGAGTATCG 604
 QY 1122 GCCACTAACCGGGGTCTCTTTCAGACACAGAGAGCATGTGGCGCCCTCTTGTCTG 1181
 DB 605 GCCACTAACCGGGGTCTCTTTCAGACACAGAGAGCATGTGGCGCCCTCTTGTCTG 664
 QY 1182 AGGGGAGCCGGGCTTCAACACACACATGCGCCCTTGAAGAGCGAGCATTTGAGCA 1241
 DB 665 AGGGGAGCCGGGCTTCAACACACACATGCGCCCTTGAAGAGCGAGCATTTGAGCA 724
 QY 1242 AAGAGAGATTAACAGAAAGACACCTCTCTAG 1276
 DB 725 AAGAGAGATTAACAGAAAGACACCTCTCTAG 759

RESULT 27
 ADH62277
 ID ADH62277 standard; cDNA; 759 BP.
 XX AC ADH62277;
 XX DT 25-MAR-2004 (first entry)
 XX DE Human PMEPAL coding cDNA.
 XX KW Androgen-regulated gene; ARG; PMEPAL; therapy; diagnosis; prognosis;
 XX KW prostate cancer; hormonal therapy; human; chromosome 20q13; gene; ss.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT CDS 1..759
 XX FT /tag= a
 XX FT /product= "Human PMEPAL protein"
 XX PN US2003170713-A1.
 XX PD 11-SEP-2003.
 XX PF 18-MAR-2003; 2003US-00390045.
 XX PR 28-JAN-2000; 2000US-0178772P.
 XX PR 31-JAN-2000; 2000US-0179045P.
 XX PR 26-JAN-2001; 2001US-00769482.
 XX PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
 XX PI Srivastava S, Moul JW, Xu LL, Segawa T;
 XX WP1; 2003-898255/82.
 XX DR P-PSDB; ADH62211.
 XX XX Polynucleotide array, useful for diagnosing or prognosing prostate
 PT cancer, comprises a planar, non-porous solid support and a set of
 PT polynucleotide probes attached to the solid support.
 XX PS Claim 10; SEQ ID NO 2; 61pp; English.
 CC The present invention relates to the identification and characterisation
 CC of a novel androgen-regulated genes (ARGs) that exhibits abundant
 CC expression in prostate tissue. The novel gene is designated PMEPAL. The
 CC invention is useful for diagnosing and prognosing prostate cancer. The
 CC invention is also useful in hormonal therapy. The present sequence is
 CC human PMEPAL coding cDNA. The PMEPAL gene is located on chromosome 20q13.
 XX SQ Sequence 759 BP; 152 A; 269 C; 226 G; 112 T; 0 U; 0 Other;

Query Match 57.2%; Score 755; DB 10; Length 759;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 755; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 522 CGAGCTGAGTTTGTTCAGATCATCATCTGTGTGTATGATGTGTGTGTG 581
 DB 5 CGAGCTGAGTTTGTTCAGATCATCATCTGTGTGTATGATGTGTGTGTG 64
 QY 582 TGAATCAGTGTCTGTGACCACTAAGCTGTTCAGAGCTTTCATCAGCCGCA 641
 DB 65 TGAATCAGTGTCTGTGACCACTAAGCTGTTCAGAGCTTTCATCAGCCGCA 124
 QY 642 GCCAGGGGGGAGAGAGAGATGCGCTGTCTCAGAGAGATGCTGTGGCCCTCGAGA 701
 DB 125 GCCAGGGGGGAGAGAGAGATGCGCTGTCTCAGAGAGATGCTGTGGCCCTCGAGA 184
 QY 702 GCACAGTGTCAAGCAACGGAATCCAGAGCCGAGGTCTAGGCCGCCCTCGAGCCCA 761
 DB 185 GCACAGTGTCAAGCAACGGAATCCAGAGCCGAGGTCTAGGCCGCCCTCGAGCCCA 244
 QY 762 ACCGCTGTGCGCCCTTTCGCCAGCGGAGGCTTTCACCGCTTTCAGCCCACT 821

XX	RESULT 30
ID	AAAA7429
AC	AAAA7429 standard; DNA; 1061 BP.
XX	
DT	20-OCT-2000 (first entry)
DE	Sequence encoding human neuron-associated protein.
XX	
KW	Neuron associated protein; NEUAP; neurological disorder; epilepsy;
KW	ischemic cerebrovascular disease; stroke; cerebral neoplasm;
KW	Alzheimer's disease; Pick's disease; Huntington's disease; dementia;
KW	Parkinson's disease; demyelinating disease; meningitis; prion disease;
KW	kuru; Creutzfeldt-Jakob disease; neurofibromatosis; cerebral palsy;
KW	mucular dystrophy; central nervous system; CNS;
KW	peripheral nervous system; PNS; myopathy; schizophrenia;
KW	actinic keratosis; arteriosclerosis; atherosclerosis; bursitis;
KW	cirrhosis; hepatitis; mixed connective tissue disease; MCTD;
KW	myelofibrosis; paroxysmal nocturnal haemoglobinuria; cancer;
KW	autoimmune disease; inflammation; acquired immunodeficiency syndrome;
KW	AIDS; Addison's disease; adult respiratory distress syndrome; allergy;
KW	amylosing spondylitis; amyloidosis; anaemia; asthma;
XX	Werner syndrome, trauma; human; ds.
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	CDS 101..859
FT	/tag= a
FT	/product= "Neuron associated protein"
PN	WO200034477-A2.
XX	
PD	15-JUN-2000.
XX	
PF	10-DEC-1999; 99MO-US030408.
PR	11-DEC-1998; 98US-00210083.
PR	09-FEB-1999; 99US-0119365P.
PR	16-MAR-1999; 99US-0124687P.
XX	
PA	(INCY-) INCYTE PHARM INC.
PI	Tang YT, Yue H, Baughn MR, Hillman JL, Lal P, Au-Young J;
PI	Yang J, Lu DM, Azimzai Y;
XX	
DR	WPI: 2000-423423/36.
XX	P-PsDB; AAB01388.
PT	New human neuron-associated proteins and polynucleotides encoding them,
PT	useful for diagnosis, treatment and prevention of cell proliferative
PT	disorders including cancer, neuronal and neurological disorders.
PS	Claim 9; Page 136; 145pp; English.
XX	
CC	Human neuron-associated proteins (NEUAP) can be used for treating or
CC	preventing a disorder associated with decreased expression or activity of
CC	NEUAP. Antagonists of NEUAP are useful for treating or preventing
CC	a disorder associated with increased expression or activity of NEUAP. NEUAP
CC	or their fragments or derivatives are useful for treating neurological
CC	disorder such as epilepsy, ischemic cerebrovascular disease, stroke,
CC	cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's
CC	disease, dementia and Parkinson's disease. NEUAPs are also useful for
CC	treating other demyelinating diseases, bacterial and viral meningitis,
CC	prion diseases including kuru, Creutzfeldt-Jakob disease, nutritional and
CC	metabolic diseases of the nervous system, neurofibromatosis, other
CC	developmental disorders of the central nervous system, cerebral palsy,
CC	neuroskelelral disorders, autonomic nervous system disorders, cranial
CC	nerv disorders, spinal cord diseases, muscular dystrophy and other
CC	neuromuscular disorders, peripheral nervous system disorders, inherited,

QY 642 GCCAGGGGGCGGAGGAGAGATGCCCTGCTCAGAGAGATGCTGTGGCCCTCGAGGA 701
DB 130 GCCAGGGGGCGGAGGAGAGATGCCCTGCTCAGAGAGATGCTGTGGCCCTCGAGGA 189
QY 702 GCACAGTGTCAAGGACAGGAATCCAGAGCCGCAAGTCTACGCCCGCTCGGCCCA 761
DB 190 GCACAGTGTCAAGGACAGGAATCCAGAGCCGCAAGTCTACGCCCGCTCGGCCCA 249
QY 762 ACCGCTGAGCCGTGCGCTCTTCCGCAAGCGGAGCGCTTCCAGCCGCTTCCAGCC 821
DB 250 ACCGCTGAGCCGTGCGCTCTTCCGCAAGCGGAGCGCTTCCAGCCGCTTCCAGCC 309
QY 822 ATCCGTACCTGACAGAGATTCACCTGCAACCCACCATCTGCTGTCAAGCGGAGG 881
DB 310 ATCCGTACCTGACAGAGATTCACCTGCAACCCACCATCTGCTGTCAAGCGGAGG 369
QY 882 AGCCCCCACTTACAGAGGCGCCCTGCAAGCTTCAAGCTTCAAGCCGCAAGCGTGG 941
DB 370 AGCCCCCACTTACAGAGGCGCCCTGCAAGCTTCAAGCTTCAAGCCGCAAGCGTGG 429
QY 942 AACTGAACCGGAGAGTGGTGGCGGCAACCCCAACAGAACCATCTTTCAGAGTGA 1001
DB 430 AACTGAACCGGAGAGTGGTGGCGGCAACCCCAACAGAACCATCTTTCAGAGTGA 489
QY 1002 TGGATAGTGCAGAGTGGGCGGCGCCCTGCAAGCTTCAAGCGGCAAGCGTGG 1061
DB 490 TGGATAGTGCAGAGTGGGCGGCGCCCTGCAAGCTTCAAGCGGCAAGCGTGG 549
QY 1062 CGTGTACGAGAGCGGCGGCGGCAAGTGAAGGCGCGCCCACTTCAAGAGGTCACTG 1121
DB 550 CGTGTACGAGAGCGGCGGCGGCAAGTGAAGGCGCGCCCACTTCAAGAGGTCACTG 609
QY 1122 GCCACTACCCGGGCTCTCTTCCAGACACAGCAGAGAGAGTGGGCGGCTTCTTGG 1181
DB 610 GCCACTACCCGGGCTCTCTTCCAGACACAGCAGAGAGAGTGGGCGGCTTCTTGG 669
QY 1182 AGGGGACCCGGCTCCACACACACATCGGCGCCCTTGAAGAGCGGCACTTGAAGCA 1241
DB 670 AGGGGACCCGGCTCCACACACACATCGGCGCCCTTGAAGAGCGGCACTTGAAGCA 729
QY 1242 AAGAGAGATTAACAGAAAGAGACCTCTCTTAAGGTCCCGAGGGGGCGGCTGGGG 1301
DB 730 AAGAGAGATTAACAGAAAGAGACCTCTCTTAAGGTCCCGAGGGGGCGGCTGGGG 789
QY 1302 CTGCTAGTGAAGAGCAG 1321
DB 790 CTGCTAGTGAAGAGCAG 809

RESULT 37
ABS61424
ID ABS61424 standard; cDNA, 1583 BP.
XX AC ABS61424;
XX DT 05-NOV-2002 (first entry)
XX DE Prostate specific nucleic acid DEX0259_32.
XX KW Human; ss; prostate specific nucleic acid; PSNA; prostate cancer;
XX KW cytosolic; non-cancerous prostate disease; PSP; vaccine;
XX KW prostate specific protein; metastasis.
OS Homo sapiens.
XX OS
XX PN WO200242776-A2.
XX PD 30-MAY-2002.
XX PF 01-NOV-2001; 2001WO-US045654.
XX PR 01-NOV-2000; 2000US-0244782P.

PA (DIAD-) DIADEXUS INC.
XX Sun Y, Recipon H, Chen S, Liu C;
PI WPI; 2002-490217/52.
XX
XX New polypeptide useful for diagnosing and monitoring the presence and
PT metastases of prostate cancer in a patient and as a component in
PT databases for search analysis as well as in sequence analysis algorithms.
PS Claim 1; Page 166-167; 242pp; English.
XX
XX The invention relates to an isolated polypeptide comprising a sequence
CC with 60 % identity to one of prostate specific protein (PSP) sequences,
CC or comprising an amino acid sequence encoded by one of 136 nucleotide
CC prostate specific nucleic acid sequences, PSNA, (or a sequence that
CC hybridises to it or is 60% identical to it), given in the specification.
CC Also included are a vector comprising the polynucleotide, a host cell
CC comprising the vector, an antibody specific for the PSP proteins and a
CC vaccine comprising the protein or polynucleotide. The PSP and PSNA are
CC useful for diagnosing and monitoring the presence and metastases of
CC prostate cancer in a patient. The PSNA is useful for determining the
CC level PSNA in a sample. An antibody to the PSP is useful for determining
CC the presence of prostate specific protein in a sample, and for treating a
CC patient with prostate cancer, which induces an immune response against
CC the prostate cancer cell expressing the nucleic acid or polypeptide and a
CC kit is useful for detecting a risk of cancer or presence of cancer in a
CC patient. PSNA is useful as hybridisation probes to detect, characterise
CC and quantify hybridising nucleic acids from both genomic and transcript-
CC derived nucleic acid samples and also in microarrays. Sequences of PSP
CC and PSNA are useful as components in databases for search analysis as
CC well as in sequence analysis algorithms. PSNA is useful to drive in vivo
CC expression of PSP. The present sequence is a PSNA of the invention
XX
SQ Sequence 1583 BP; 361 A; 469 C; 457 G; 296 T; 0 U; 0 Other;
Query Match 42.4%; Score 560; DB 6; Length 1583;
Best Local Similarity 100.0%; Pred. No. 3.7e-240;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 730 GCCGAGGTCTACGCGCCGCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 789
DB 827 GCCGAGGTCTACGCGCCGCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 886
QY 790 GCCGAGCGCTTCCAGCGGCTTCCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 849
DB 887 GCCGAGCGCTTCCAGCGGCTTCCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 946
QY 850 GCCACCCACCATCTGCTGTCAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 909
DB 947 GCCACCCACCATCTGCTGTCAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1006
QY 910 CTTCCAGCTTCCGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 969
DB 1007 CTTCCAGCTTCCGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1066
QY 970 CCAAAAGAGAGATCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1029
DB 1067 CCAAAAGAGAGATCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1126
QY 1030 CCCCCCAGAGATTAAGTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1089
DB 1127 CCCCCCAGAGATTAAGTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1186
QY 1090 GGGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1149
DB 1187 GGGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1246
QY 1150 CCAGCAGAGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1209
DB 1247 CCAGCAGAGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1306
QY 1210 CCGGCGCGCTTGAAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1269

QY 913 CCAGCTTCGGAGACCCCGAGCAGCAGCTGGAACCTGACCGGAGTGTGCGGCGACCCCC 972
 DB 564 CCAGCTTCGGAGACCCCGAGCAGCAGCTGGAACCTGACCGGAGTGTGCGGCGACCCCC 505
 QY 973 AAACGAAACCATCTTTCGACAGTACCTGATGTGTGACGCTGCGGCGCCCTGCCC 1032
 DB 504 AAACGAAACCATCTTTCGACAGTACCTGATGTGTGACGCTGCGGCGCCCTGCCC 445
 QY 1033 CCCGAGTAAGTACGCGGATCAGCGCCACGTCGTACAGCGACGCGCGCGCATGAGAG 1092
 DB 444 CCCGAGTAAGTACGCGGATCAGCGCCACGTCGTACAGCGACGCGCGCGCATGAGAG 385
 QY 1093 GCGCGCGG-CGCCAGTACAGCAGGTCATGCGCCACTACCCCGGGGTCTCTTCAGCAGC 1151
 DB 384 GCGCGCGGCGCCAGTACAGCAGGTCATGCGCCACTACCCCGGGGTCTCTTCAGCAGC 325
 QY 1152 AGCAGAGCAGTGGGCGCGCTCTTCTGAGAGGAGACCCGCGCTCCACACACACATCG 1211
 DB 324 AGCAGAGCAGTGGGCGCGCTCTTCTGAGAGGAGACCCGCGCTCCACACACACATCG 265
 QY 1212 GCGCCCTAGAGAGCGCAGCAGCTCTGAGAGCAAGAGATTAAGAGAGACACCTTC 1271
 DB 264 GCGCCCTAGAGAGCGCAGCAGCTCTGAGAGCAAGAGATTAAGAGAGACACCTTC 205
 QY 1272 TCTAGAGTCCCGAGGAGGCGCGGCTGAGGCTGCGTGGTGAAGAGCAG 1321
 DB 204 TCTAGAGTCCCGAGGAGGCGCGGCTGAGGCTGCGTGGTGAAGAGCAG 155

RESULT 43
 AB284732/c
 ID AB284732 standard; cDNA; 474 BP.

XX AC AB284732;
 XX DT 14-MAY-2003 (first entry)
 XX DE Toxicologically relevant human nucleotide sequence #1891.
 XX DE Toxicologically relevant gene; toxicological response; gene; ss.
 XX KW Homo sapiens.
 XX OS
 XX PN MO2003016500-A2.
 XX PD 27-FEB-2003.
 XX PF 16-AUG-2002; 2002MO-US026514.
 XX PR 16-AUG-2001; 2001US-0313080P.
 XX PA (PHASE-) PHASE-1 MOLECULAR TOXICOLOGY INC.
 XX PI Neft RE, Dunn RT, Adkins K, Pickett GG, Kier LD, Schneider K;
 XX PI Alen P;
 XX DR WPI; 2003-268322/26.
 XX PT Determining a toxicological response to an agent, useful for screening of
 XX PT drug, comprises comparing the expression profile of one or more human
 XX PT toxic response genes to a reference gene expression profile indicative of
 XX PT toxicity.
 XX PS Claim 1; Page 444; 455pp; English.
 XX CC The present invention describes a method (M1) for determining a
 XX CC toxicological response to an agent, which comprises comparing the
 XX CC expression profile of one or more human toxic response genes to a
 XX CC reference gene expression profile indicative of toxicity, and so
 XX CC determining the presence of a toxic response to the agent. Also
 XX CC described: (1) an array comprising one or more polynucleotides selected
 XX CC from the genes corresponding to the partial sequences given in AB282842

CC to AB284764, or their fragments of at least 20 nucleotides, or homologues
 CC ; and (2) determining if a gene putatively identified to be a toxic
 CC response gene plays a role on toxic response pathways by determining the
 CC expression profile of the gene after exposure of cells or a human subject
 CC to a known toxic pharmaceutical or industrial agent, comprising: (a)
 CC exposing cells to an agent; (b) obtaining the test gene expression profile
 CC for a putatively identified toxic response gene after exposure to a known
 CC toxic pharmaceutical or industrial agent; and (c) comparing the test
 CC profile to the expression profile of a gene with a similar function or
 CC comparing the test profile to the expression profile of that gene after
 CC exposure to other known toxic compounds. The methods are useful for
 CC predicting and determining toxicological responses on a cellular, organ
 CC or system level. The arrays comprising the human genes are useful for
 CC toxicological screening of drugs, pharmaceutical compounds and chemicals
 SQ

Query Match 27.6%; Score 364; DB 10; Length 474;
 Best Local Similarity 99.8%; Pred. No. 1.9e-152;
 Matches 414; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 714 GCACGAGATCCAGAGCGGAGGTACGCGCCGCTGCGCCACCGAGCTGGCG 773
 DB 474 GCACGAGATCCAGAGCGGAGGTACGCGCCGCTGCGCCACCGAGCTGGCG 415
 QY 774 TCGCGCCCTTGGCCAGCGGAGCGCTTCCACCGCTTCCAGCCCACTATCGTACGCG 833
 DB 414 TCGCGCCCTTGGCCAGCGGAGCGCTTCCACCGCTTCCAGCCCACTATCGTACGCG 355
 QY 834 AGCAGAGATGAGACCTGACACCCACCATCTGCTGTACAGCGGAGAGAGCCCACTCT 893
 DB 354 AGCAGAGATGAGACCTGACACCCACCATCTGCTGTACAGCGGAGAGAGCCCACTCT 295
 QY 894 ACCAGAGCCCTGACACCTTCCAGCTTGGAGACCCCGAGCAGAGCTGGAACCTGAACCGG 953
 DB 294 ACCAGAGCCCTGACACCTTCCAGCTTGGAGACCCCGAGCAGAGCTGGAACCTGAACCGG 235
 QY 954 AGTCGCTGGCGGACACCCCAACAGACATCTTGGACAGTACCTGATGATAGTGGCA 1013
 DB 234 AGTCGCTGGCGGACACCCCAACAGACATCTTGGACAGTACCTGATGATAGTGGCA 175
 QY 1014 GCGTGGGCGGCGCCCGCCCGCCAGCAGTAAGTGGGATCAGCCGCACTGCTACGGCA 1073
 DB 174 GCGTGGGCGGCGCCCGCCCGCCAGCAGTAAGTGGGATCAGCCGCACTGCTACGGCA 115
 QY 1074 GCGGCGGCGGATGAGAGGCGCGCCGACCTACAGCAGAGTCAATGGCCACTA 1128
 DB 114 GCGGCGGCGGATGAGAGGCGCGCCGACCTACAGCAGAGTCAATGGCCACTA 60

RESULT 44
 ABK12143/c
 ID ABK12143 standard; cDNA; 693 BP.
 XX AC ABK12143;
 XX DT 05-JUN-2002 (first entry)
 XX DE Human MIVR-1 homologous sequence #1.
 XX KW Human; ss; MIVR-1; Mechanically induced Vascular Receptor 1; cytosolic;
 XX KW cardiant; cerebroprotective; antiarteriosclerotic; cardiac cell;
 XX KW anti-apoptotic; vascular endothelial cell; cardiac hypertrophy;
 XX KW myocardial infarction; stroke; arteriosclerosis; heart failure;
 XX KW AI761441.1.
 XX OS Homo sapiens.
 XX OS
 XX PN MO200216416-A2.
 XX PD 28-FEB-2002.

PF 21-AUG-2001; 2001WO-US026089.
XX
XX 22-AUG-2000; 2000US-0227159P.
XX
XX (BGM) BRIGHAM & WOMENS HOSPITAL INC.
XX (PIZ) PIZER INC.
XX
XX Lee RT, Landeschulz KT, Kennedy SP, Thompson JF, Turi TG;
XX WPI; 2002-280912/32.
XX
XX Novel nucleic acid molecule encoding Mechanically Induced Vascular
XX Receptor-1 polypeptide, useful for treating cardiovascular diseases.
XX
XX Disclosure; Page 101; 105pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule encoding a
XX Mechanically Induced Vascular Receptor (MIVR)-1 polypeptide having
XX cardiac cell anti-apoptotic activity and fragments of it provided they
XX are not identical to Genbank sequences A1761441.1, A1594390, NM_004338
XX and A0177461. Also included are expression vectors, host cells, the MIVR-
XX 1 polypeptide, MIVR-1 binding peptides, modulators of MIVR-1, contacting
XX a molecule having cardiac cell anti-apoptotic activity with a candidate
XX agent, where the molecule is a nucleic acid molecule comprising MIVR-1,
XX IEX-1, VDRP-1, BRG-2 and TIS-11d or its expression product, determining
XX if the anti-apoptotic activity is modulated and thereby identifying a
XX modulator. The cardiac cell anti-apoptotic molecules and nucleic acids
XX of the invention are useful for treating, diagnosing and monitoring
XX progression of such diseases and disorders as characterised by increased
XX apoptotic cell-death of vascular endothelial cells e.g. cardiac
XX hypertrophy, myocardial infarction, stroke, arteriosclerosis and heart
XX failure. The present sequence is one of the four Genbank sequences
XX (A1761441.1) which are homologous to the cDNA for human MIVR-1 and which
XX are specifically disclaimed
XX
SQ Sequence 693 BP; 101 A; 205 C; 237 G; 149 T; 0 U; 1 Other;

Query Match 22.9%; Score 302; DB 6; Length 693;
Best Local Similarity 100.0%; Pred. No. 9.8e-125;

Matches 302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 885 CCCACCTTACAGAGGCCCCCTGACCTTCAGAGCTTGGGAGCCCGAGAGCAGCTGAGAC 944
DB 587 CCCACCTTACAGAGGCCCCCTGACCTTCAGAGCTTGGGAGCCCGAGAGCAGCTGAGAC 528
QY 945 TGAACCGGAGTGGGTGGCGGACCCCAACAGAACATCTTCAGACAGTGAAGCTGATGG 1004
DB 527 TGAACCGGAGTGGGTGGCGGACCCCAACAGAACATCTTCAGACAGTGAAGCTGATGG 468
QY 1005 ATAGTGCAGAGGTGGGTGGCGGACCCCAACAGAACATCTTCAGACAGTGAAGCTGATGG 1064
DB 467 ATAGTGCAGAGGTGGGTGGCGGACCCCAACAGAACATCTTCAGACAGTGAAGCTGATGG 408
QY 1065 GCTACGGAGCGGCGGAGCATGAGAGGCGCGCCCACTTACAGAGCAGTGCATCGGC 1124
DB 407 GCTACGGAGCGGCGGAGCATGAGAGGCGCGCCCACTTACAGAGCAGTGCATCGGC 348
QY 1125 ACTACCGGAGTCTCTTCAGACACAGCAGAGCAGTGGGCGGCTCTTCAGAGG 1184
DB 347 ACTACCGGAGTCTCTTCAGACACAGCAGAGCAGTGGGCGGCTCTTCAGAGG 288
QY 1185 GG 1186
DB 287 GG 286

RESULT 45

AAZ52964 standard; cDNA; 812 BP.

AAZ52964;

14-MAR-2000 (first entry)

XX
XX Human prostate tumor cDNA library derived EST fragment #107.
XX
XX Pancreas; tumor; EST; expressed sequence tag; human; cytosolic;
XX treatment; ds.
XX
XX Homo sapiens.
XX
XX DE19820190-A1.
XX
XX 04-NOV-1999.
XX
XX 28-APR-1998; 98DE-01020190.
XX
XX 28-APR-1998; 98DE-01020190.
XX
XX (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
XX Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
XX WPI; 1999-621386/54.
XX P-PSDB; AAY74135, AAY74136, AAY74137.
XX
XX New human nucleic acid sequences from pancreatic tumors, and related
XX proteins.
XX
XX Claim 2; Page 269-270; 502pp; German.
XX
XX This invention describes novel polypeptides and their encoding nucleic
XX acids derived from human pancreatic tumor tissue which have cytostatic
XX activity. The sequences are also useful in producing pharmaceutical
XX compositions for treatment of pancreatic tumors. AAZ52858-253014
XX represent expressed sequence tag (EST) fragments derived from a human
XX pancreatic tumor cDNA library and which encode the proteins represented
XX in AAY73814-Y74252
XX
SQ Sequence 812 BP; 157 A; 272 C; 237 G; 146 T; 0 U; 0 Other;

Query Match 20.5%; Score 271; DB 2; Length 812;
Best Local Similarity 99.7%; Pred. No. 7.2e-111;

Matches 321; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 585 TCAGTGTCTGTAGAGCAGTACAGAGCTGTGTGACGAGTCTTTCATGACCGGACAGCC 644
DB 426 TCAGTGTCTGTAGAGCAGTACAGAGCTGTGTGACGAGTCTTTCATGACCGGACAGCC 485
QY 645 AGGGGCGAGAGAGAAAGATGCTGTCTTCAGAAAGATGCTGTGAGCTTGGAGAGCA 704
DB 486 AGGGGCGAGAGAGAAAGATGCTGTCTTCAGAAAGATGCTGTGAGCTTGGAGAGCA 545
QY 705 CAGTGTCAAGGCAAGGAATCCCAAGCCGAGGTCTTACGCCCCGCTTCGCGCACCGACC 764
DB 546 CAGTGTCAAGGCAAGGAATCCCAAGCCGAGGTCTTACGCCCCGCTTCGCGCACCGACC 605
QY 765 GCTGAGCGGTGCGGCTTTCAGAGCGGAGCGCTTTCAGAGCGCTTTCAGAGCGCTTTCAGAGCG 824
DB 606 GCTGAGCGGTGCGGCTTTCAGAGCGGAGCGCTTTCAGAGCGCTTTCAGAGCGCTTTCAGAGCG 665
QY 825 CGTACTGACAGCAGAGTGCACCTGCGCACCCACATCTGTCTGTCAAGCGGAGAGAGC 884
DB 666 CGTACTGACAGCAGAGTGCACCTGCGCGCCACCATCTGTCTGTCAAGCGGAGAGAGC 725
QY 885 CCCACCTTACAGAGGCGGCTTTCAGAGCGGAGCGCTTTCAGAGCGCTTTCAGAGCGCTTTCAGAGCG 906
DB 726 CCCACCTTACAGAGGCGGCTTTCAGAGCGGAGCGCTTTCAGAGCGCTTTCAGAGCGCTTTCAGAGCG 747

RESULT 46

AAA41265 standard; cDNA; 254 BP.

AAA41265;

XX

XX 21-AUG-2000 (first entry)
DE Human secreted expressed sequence tag SEQ ID NO:5.
XX Human; mouse; xenopus; rat; secreted expressed sequence tag; sEST;
XX expressed sequence tag; EST; probe; chemotactic; proliferative;
XX immunomodulatory; haematopoietic; chemokine; analgesic; haemostatic;
XX thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal;
XX antiviral; antidiabetic; antisthmatic; vulnery; antiparkinsonian;
XX anticulcer; osteopathic; neuroprotective; nootropic; antipsoriatic;
XX cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine;
XX autoimmune disorder; multiple sclerosis; allergic condition;
XX insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
XX lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
XX central nervous system disorder; Alzheimer's disease; stroke;
XX Parkinson's disease; Huntington's disease; coagulation disorder;
XX haemophilia; thrombosis; inflammatory disorder; Crohn's disease; tumour;
XX infection; depression; psoriasis; ss.
OS Homo sapiens.
XX
XX WO200021990-A1.
XX
XX 20-APR-2000.
XX
XX 15-OCT-1999; 99WO-US024205.
XX
XX 15-OCT-1998; 98US-0104435P.
XX
XX (GENY) GENNETICS INST INC.
XX
XX Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
XX Merberg D, Treacy M;
XX WPI, 2000-317937/27.
XX
XX Isolated polynucleotides, and encoded proteins, comprising secreted
XX expressed sequence tags (sESTs), useful for treating various disorders
XX such as autoimmune, infectious, and central nervous system disorders.
XX
XX
XX Claim 1; Page 180; 618pp; English.
XX
XX AAA1261 to AAA43419 represent specifically claimed secreted expressed
XX sequence tags (sESTs), isolated from human, mouse, xenopus and rat tissue
XX sources. The sESTs can have a range of activities depending on the
XX tissues they were isolated from. The activities include: chemotactic;
XX proliferative; immunomodulatory; haematopoietic; chemokine; analgesic;
XX haemostatic; thrombolytic; antiinflammatory; cytostatic; antibacterial;
XX antifungal; antiviral; antidiabetic; antisthmatic; vulnery; anticulcer;
XX osteopathic; neuroprotective; nootropic; antiparkinsonian; antipsoriatic;
XX cerebroprotective; anticonvulsant; and antidepressant. The sESTs can be
XX used for gene therapy and in vaccines. The sESTs are useful as probes for
XX the identification and isolation of full-length cDNAs and genomic DNA
XX molecules which correspond to the sESTs. Proteins encoded by the sESTs
XX are useful in assays for determining biological activity and raising
XX antibodies. They may be useful for treatment of autoimmune disorders
XX (multiple sclerosis, insulin dependent diabetes), allergic conditions
XX (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,
XX osteoporosis, osteoarthritis, central nervous system disorders
XX (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
XX disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's
XX disease), tumours, bacterial, fungal or viral infections, depression and
XX psoriasis. AAA43420 to AAA43425 represent linker variants which are given
XX in the exemplification of the present invention
XX
XX Sequence 254 BP; 46 A; 85 C; 82 G; 41 T; 0 U; 0 Other;
XX
XX Query Match 17.3%; Score 229; DB 3; Length 254;
XX Best Local Similarity 100.0%; Pred. No. 4,7e-92;
XX Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX

[illegible]

XX Homo sapiens.
OS
XX US2003073623-A1.
PN
XX 17-APR-2003.
PD
XX 30-JUL-2001; 2001US-00918995.
PF
XX 30-JUL-2001; 2001US-00918995.
PR
XX 30-JUL-2001; 2001US-00918995.
XX
XX (DRMANAC R T.
PA (LABAT I.
PA (STACHE-CRAIN B.
PA (DICKSON M C.
PA (JONES L W.
XX
PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX
XX WPI; 2003-615964/58.
XX
XX
XX New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX
XX
XX Claim 1; SEQ ID NO 2074; 44bp; English.
XX
XX The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversity, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC segdata.uspto.gov/sequence.html?DocID=20030073623
XX
SQ Sequence 467 BP; 133 A; 121 C; 131 G; 74 T; 0 U; 8 Other;
Query Match 13.5%; Score 178; DB 9; Length 467;
Best Local Similarity 100.0%; Pred. No. 3e-69;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1144 CCAGCACCCGACGAGAGTGGCGCCCTCTGCTGAGAGGGACCCGGCTCCACACAC 1203
DB 36 CCAGCACCCGACGAGAGTGGCGCCCTCTGCTGAGAGGGACCCGGCTCCACACAC 95
QY 1204 ACACATCGCGCCCTGAGAGGCGCAGCATCTGAGCAAGAAAGATTAACAGAAAG 1263
DB 96 ACACATCGCGCCCTGAGAGGCGCAGCATCTGAGCAAGAAAGATTAACAGAAAG 155
QY 1264 ACACCTCTCTAGAGTCCCGAGGGGGCGGGCTGGGGCTGCGTAGGTAAAAAGGCGAG 1321
DB 156 ACACCTCTCTAGAGTCCCGAGGGGGCGGGCTGGGGCTGCGTAGGTAAAAAGGCGAG 213

Search completed: February 28, 2006, 10:42:32
Job time : 826 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2006, 10:02:46, Search time 5833 Seconds
(without alignments)
10595.874 Million cell updates/sec

Title: US-09-934-249-1

Perfect score: 1321

Sequence: 1 cgaccgcggtctcggagcga.....ctcgtaggtcgaagcag 1321

Scoring table: OLIGO NUC
Gapop 60.0, Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size: 23

Total number of hits satisfying chosen parameters: 16459

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

Database:

EST:
1: gb_est1:
2: gb_est2:
3: gb_est3:
4: gb_hic:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_est7:
9: gb_gsa1:
10: gb_gsa2:
11: gb_gsa3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	741	56.1	901	4	CR612083
2	632	47.8	1046	3	BM9222276
3	614	46.5	967	5	BQ641849
4	588	44.5	647	8	DN9923232
5	588	43.0	916	5	BQ954555
6	558	42.2	609	5	BQ636742
7	542	41.6	551	3	BM141979
8	542	41.0	601	8	DN991959
9	536	40.6	605	7	CV028567
10	533	40.3	850	1	AL558881
11	518	39.2	729	5	BQ575741
12	511	38.7	850	5	BQ602918
13	497	37.6	890	5	BQ607050
14	495	37.5	553	8	DN990606
15	474	35.9	572	5	BK641317
16	471	35.7	1068	5	BUS27705
17	468	35.4	655	5	BQ681705
18	450	34.1	964	5	BQ859860
19	449	34.0	945	5	BUS39219
20	445	33.7	782	3	BQ015170
21	442	33.5	602	6	CA431191
22	442	33.5	780	10	AY19334

23	441	33.4	461	3	BM712680
24	437	33.1	633	3	BM714472
25	428	32.4	588	5	BQ624784
26	425	32.2	897	1	AL558882
27	424	32.1	1038	1	AL517150
28	422	31.9	844	5	BQ686793
29	422	31.9	938	5	BUI57842
30	422	31.9	952	5	BUI57959
31	422	31.9	1280	5	BQ691500
32	417	31.6	559	2	BE855409
33	417	31.6	629	5	BUI730650
34	406	30.7	1400	3	BM559329
35	401	30.4	730	3	BM677602
36	399	30.2	626	3	BM974296
37	395	29.9	544	7	CN296134
38	393	29.8	728	5	BQ683523
39	390	29.5	973	5	BUI69156
40	383	29.0	570	5	BQ575582
41	377	28.5	563	6	CB049800
42	365	27.6	552	3	BM713900
43	358	27.1	1127	5	BUI74654
44	348	26.3	646	5	BQ859841
45	338	25.6	867	5	BX362396
46	331	25.1	899	5	BUI96912
47	327	24.8	547	3	BM676516
48	324	24.5	613	2	BG680325
49	302	22.9	651	6	CB554226
50	302	22.9	693	1	AI761441
51	291	22.0	502	1	AI921394
52	288	21.8	668	6	CB044866
53	286	21.7	446	3	BM681946
54	283	21.4	437	1	AI936228
55	280	21.2	990	5	BQ691066
56	277	21.0	277	6	CB108549
57	268	20.3	618	6	CD367193
58	257	19.5	308	3	BM705514
59	246	18.6	451	1	AI493698
60	243	18.4	518	1	AI885001
61	239	18.1	453	1	AA917446
62	239	18.1	588	1	AI377498
63	239	18.1	619	1	AI742327
64	235	17.8	380	2	BE138909
65	232	17.6	705	6	CA418897
66	230	17.4	284	2	AM452945
67	225	17.0	397	2	BF46904
68	225	17.0	430	1	AM204238
69	225	17.0	463	2	BF939262
70	225	17.0	463	5	BUI739449
71	225	17.0	674	1	AI972096
72	224	17.0	468	5	BX352377
73	222	16.8	381	1	AM135998
74	222	16.8	1264	5	BQ877825
75	221	16.7	489	1	AI921217
76	218	16.5	453	1	AI467828
77	218	16.5	457	1	AI369306
78	217	16.4	464	2	AI928027
79	216	16.4	404	1	AI928027
80	216	16.4	889	5	BQ883225
81	215	16.3	524	1	AI640802
82	209	15.8	242	3	BM767985
83	208	15.7	221	3	BM768155
84	198	15.0	624	2	BG897912
85	198	15.0	990	2	BQ675643
86	197	14.9	342	1	AI521341
87	196	14.8	338	6	CB144148
88	194	14.7	634	1	AI826012
89	188	14.2	508	1	AA595115
90	179	13.6	467	1	AA007283
91	177	13.4	438	1	AA088701
92	175	13.2	857	2	BG323347
93	174	13.2	472	5	BUI732052
94	171	12.9	454	1	AA027926
95	160	12.1	386	2	BF475759

BM712680	UI-E-E30-
BM714472	UI-E-E30-
BQ624784	UI-H-RG1-
AL558882	AL558882
AL517150	AL517150
BQ686793	AGENCOURT
BUI57842	AGENCOURT
BUI57959	AGENCOURT
BQ691500	AGENCOURT
BE855409	UI-E-E30-
BUI730650	UI-E-E30-
BM559329	AGENCOURT
BM677602	UI-E-E30-
BM974296	UI-E-E30-
CN296134	UI-E-E30-
BQ683523	UI-E-E30-
BUI69156	AGENCOURT
BQ575582	UI-H-E21-
CB049800	NISC 9113
BM713900	UI-E-E30-
BUI74654	AGENCOURT
BQ859841	AGENCOURT
BX362396	BX362396
BUI96912	AGENCOURT
BM676516	UI-E-E30-
BG680325	602629217
CB554226	MSBP0052
AI761441	W955F07.X
AI921394	W024C07.X
CB044866	NISC 9C07
BM681946	UI-E-E30-
AI936228	W03E04.X
BQ691066	AGENCOURT
CB108549	K-E30T148
CD367193	UI-H-E30-
BM705514	UI-E-E30-
AI493698	QY97C07.X
AI885001	W188C11.X
AA917446	O151D08.X
AI377498	LC37C07.X
AI742327	W950F07.X
BE138909	XW97F09.X
CA418897	UI-H-E21-
AM452945	UI-H-E21-
BF46904	7065C12.X
AM204238	UI-H-B11-
BF939262	nad86D06.
BUI739449	UI-E-E30-
AI972096	W162D11.X
BX352377	BX352377
AM135998	UI-H-B11-
BQ877825	AGENCOURT
AI921217	W021H12.X
AI467828	C178D03.X
AI369306	QY91E08.X
BQ883225	AGENCOURT
AI640802	C171G09.X
BM767985	K-E30T051
BM768155	K-E30T051
BG897912	HOA26-1-B
BQ675643	603622053
AI521341	C105B09.X
CB144148	W429G04.X
AI826012	W429G04.X
AA595115	nc32D02.8
AA007283	W54E08.X
AA088701	Z183F05.8
BG323347	602421734
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AA027926	ZK05H07.X
BF475759	nac41D07.

C 96 157 11.9 353 1 AM073519
C 97 155 11.7 377 1 A1336269
98 151 11.4 198 3 BM763156
99 148 11.2 1242 5 BQ689488
100 147 11.1 147 7 CN288822
C 101 146 11.1 339 1 AA953976
102 146 11.1 381 1 AL732104
103 146 11.1 287 10 AY419335
C 104 143 10.8 297 1 A1474392
C 105 141 10.7 413 1 A1039567
C 106 141 10.7 423 1 AA126899
C 107 134 10.1 540 1 A1804815
108 134 10.1 1059 1 A1543170
109 127 9.6 361 1 AA310984
C 110 124 9.4 344 1 A1537597
111 123 9.3 175 3 BM846677
C 112 119 9.0 1005 1 A1578575
C 113 117 8.9 520 3 BM142517
C 114 113 8.6 454 2 BG059801
C 115 112 8.5 388 5 BX344440
C 116 111 8.4 279 3 BM684448
117 110 8.3 711 7 CF028468
118 110 8.3 900 2 BF036086
C 119 108 8.2 287 6 CB049799
120 108 8.2 1017 5 BU846262
C 121 107 8.1 220 2 BE835168
122 105 7.9 243 3 BE770348
C 123 104 7.9 289 3 BM930946
C 124 104 7.9 301 1 AM135709
125 99 7.5 369 1 AA088767
126 95 7.2 1427 3 BM912387
C 127 87 6.6 641 1 AN071693
128 86 6.5 195 1 AA128075
C 129 84 6.4 484 1 A1905464
130 81 6.1 161 1 AL732107
C 131 79 6.0 221 2 BE672926
132 78 5.9 191 1 AL732106
133 76 5.8 178 6 CB133781
134 72 5.5 354 1 AL732105
C 135 72 5.3 351 1 AA027860
C 136 70 4.9 458 1 AV611581
137 65 4.9 351 1 AA249792
138 63 4.8 208 1 AA249792
139 62 4.7 1480 3 BM926155
C 140 61 4.6 791 3 BM006868
141 59 4.5 265 1 AA570597
142 59 4.5 318 1 AA536113
143 58 4.4 218 8 N71820
144 58 4.4 284 1 AA535181
145 57 4.3 436 3 BM482193
146 57 4.3 467 2 BE666930
147 57 4.3 509 1 AA656282
148 57 4.3 548 6 CB460475
149 57 4.3 588 3 BM483503
150 57 4.3 642 6 CB455288
C 151 56 4.2 134 1 A1251117
C 152 56 4.2 333 1 AM050740
C 153 56 4.2 347 1 AA559064
154 56 4.2 522 1 AA535819
155 55 4.2 245 8 DN933581
156 55 4.2 219 1 A1936108
C 157 48 3.6 152 1 A1865867
158 48 3.6 191 1 A1623933
159 47 3.6 365 1 AW315093
C 160 45 3.6 492 6 CB044865
161 45 3.4 491 3 BM767932
162 44 3.3 287 2 BE646987
163 44 3.3 287 10 CG481614
164 44 3.3 293 2 BG088400
165 44 3.3 324 2 BE136876
166 44 3.3 329 10 CG655913
167 44 3.3 340 5 BQ566498
168 44 3.3 349 10 CG625117

AM073519 ka36h06.x
A1336269 qf45d08.x
BM763156 K-EST0044
BQ689488 AGENCOURT
CN288822 170005998
AA953976 coo8h09.8
AL732104 AL732104
AY419335 Pan tco01
A1474392 ch19f03.x
A1039567 ox37f07.s
AA126899 z116d08.8
A1804815 EX03c11.x
A1543170 AL543170
AA310984 EST181777
A1537597 lp05b05.x
BM846677 K-EST0125
A1578575 AL578575
BM142517 lf35c05.x
BG059801 naf15c10.
BX344440 BX344440
BM684448 UI-E-EIO-
CJ028468 CJ028468
BF036086 601458441
CB049799 NISC 9113
BU846262 AGENCOURT
BE835168 RCS-FN002
BE770348 PMO-FT005
BM930946 UI-E-EIO-
AM135709 UI-H-B11-
AA088767 z183f05.x
BM912387 w653c08.x
AN071693 AGENCOURT
AA128075 z116d08.x
A1905464 RC-BT091-
AL732107 AL732107
BE672926 7d25f07.x
AL732106 AL732106
CB133781 K-EST0184
AL732105 AL732105
AW673569 xv67d07.x
AA027860 k205h07.s
AV611581 AV611581
AA249792 19623.8eq
BM926155 AGENCOURT
BM006868 603615341
AA570597 nj82907.s
AA536113 nj81e05.s
AA535181 nj75b01.s
N71820 yz29g10.r1
AA535181 nj75b01.s
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BE666930 108453 MA
AA656282 108453 MA
CB460475 720364 MA
BM483503 536869 MA
CB455288 712422 MA
A1251117 Gx50b12.x
AM050740 w220f03.x
AA559064 n15e12.s
AA535819 nj79e01.s
DN933581 L1B8934-0
A1936108 wo61g10.x
A1865867 wk87d05.x
A1623933 t640d05.x
AW315093 11928 MAR
CB044865 NISC gsc07
BM767932 K-EST0050
BE646987 UI-M-BH1-
CG481614 OST14172
BG088400 H3152F10-
BE136876 ug56h05.y
CG655913 OST427197
BQ566498 g161906.y
CG625117 OST329985

169 44 3.3 429 8 CV891486
170 44 3.3 446 10 CG513056
C 171 44 3.3 445 1 AM557419
C 172 44 3.3 464 3 B1407324
173 44 3.3 487 10 CG505306
174 44 3.3 487 10 CG517246
175 44 3.3 489 10 CG499064
176 44 3.3 492 10 CG676530
177 44 3.3 496 10 CG621781
178 44 3.3 497 10 CG659330
179 44 3.3 499 10 CG651747
180 44 3.3 501 10 CG651819
181 44 3.3 509 10 CG612326
182 44 3.3 521 10 CG655775
183 44 3.3 547 10 CG652576
184 44 3.3 565 2 BG075859
185 44 3.3 600 6 CA529349
186 44 3.3 623 2 B1107222
187 44 3.3 624 10 AY419336
188 44 3.3 638 1 AJ743741
189 44 3.3 646 10 CG784326
190 44 3.3 841 2 B1156703
191 44 3.3 894 3 B1851941
192 44 3.3 1207 4 AK008976
193 42 3.2 296 6 CB701767
194 42 3.2 438 7 BF547056
195 42 3.2 686 7 CN543620
196 41 3.1 352 2 BE457294
197 41 3.1 380 2 BF193018
198 41 3.1 402 1 A1466182
199 41 3.1 451 1 AJ681929
200 41 3.1 475 1 A1594390
201 41 3.1 582 2 BE553323
202 41 3.1 637 5 EX917028
203 41 3.1 718 3 BQ205733
204 41 3.1 719 3 B1692342
205 41 3.1 914 6 CB183931
206 41 3.1 974 2 BB624904
207 39 3.0 10 CG514861
208 39 3.0 429 10 CG494876
209 39 3.0 663 2 BB645391
210 38 2.9 260 1 AM572959
211 38 2.9 455 10 CG497753
212 38 2.9 685 7 CK830782
213 37 2.8 505 1 AJ451145
214 37 2.8 515 1 AM670986
215 37 2.8 720 10 CW299727
216 36 2.7 481 1 AJ743736
217 35 3.32 2 BF200804
218 34 2.6 112 9 BQ209428
219 34 2.6 325 1 AJ449342
220 34 2.6 347 8 DN752530
221 34 2.6 384 1 AA472643
222 34 2.6 456 2 BE474205
223 34 2.6 456 8 DN271310
224 34 2.6 462 9 BH018731
225 34 2.6 478 2 BE474221
226 34 2.6 504 2 BG510825
227 34 2.6 521 8 CX596278
228 34 2.6 535 1 AL819414
229 34 2.6 548 6 CD668079
230 34 2.6 554 6 CA939087
231 34 2.6 884 8 CX109179
232 34 2.6 884 8 CX109179
233 33 3.3 351 1 A1481514
234 33 2.5 351 1 A1481514
235 33 2.5 650 7 CN204183
236 32 2.4 125 10 CL178675
237 32 2.4 313 5 B1149073
238 32 2.4 324 5 BY778806
239 32 2.4 326 5 BY782199
240 32 2.4 328 5 B143859
241 32 2.4 329 5 BY790136

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CG505306 OST54204
CG517246 OST77408
CG499064 OST40901
CG676530 OST461597
CG659330 OST320556
CG621781 OST30565
CG659290 OST45359
CG651747 OST413539
CG651819 OST413770
CG612326 OST298421
CG655775 OST46764
CG652576 OST32546
BG075859 H1152F10-
CA529349 8103-25 M
B1107222 602894178
AY419336 Mus muscu
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AK008976 Mus muscu
CB701767 AMGNMUC:M
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BF193018 244447 MA
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AJ681929 AJ681929
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CW299727 LG1 782_1
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C 242	32	2.4	329	8	DN141366	DN141366	5013	G09	C 315	31	2.3	481	1	AU076124	AU076124
243	32	2.4	331	5	BY780596	BY780596			C 316	31	2.3	481	7	CR285442	CR285442
244	32	2.4	333	5	BY147191	BY147191			C 317	31	2.3	486	7	CV725225	CV725225
245	32	2.4	333	5	BY148003	BY148003			C 318	31	2.3	486	7	CV733924	CV733924
246	32	2.4	334	5	BY148431	BY148431			C 319	31	2.3	488	7	CV728654	CV728654
247	32	2.4	335	5	BY144425	BY144425			C 320	31	2.3	489	7	CV725222	CV725222
248	32	2.4	338	5	BY788377	BY788377			C 321	31	2.3	491	7	CV734202	CV734202
249	32	2.4	338	5	BY793575	BY793575			C 322	31	2.3	500	8	DN434218	DN434218
250	32	2.4	340	5	BY144643	BY144643			C 323	31	2.3	515	1	AU165639	AU165639
251	32	2.4	342	5	BY136577	BY136577			C 324	31	2.3	522	7	CV728787	CV728787
252	32	2.4	343	5	BY776061	BY776061			C 325	31	2.3	525	6	CV7319361	CV7319361
253	32	2.4	350	5	BY789853	BY789853			C 326	31	2.3	528	7	CV734094	CV734094
254	32	2.4	353	5	BY147361	BY147361			C 327	31	2.3	534	6	CV7298163	CV7298163
255	32	2.4	354	5	BY781381	BY781381			C 328	31	2.3	530	6	CV7334309	CV7334309
256	32	2.4	355	5	BY776804	BY776804			C 329	31	2.3	531	6	CV7281296	CV7281296
257	32	2.4	356	5	BY788868	BY788868			C 330	31	2.3	531	6	CV7311716	CV7311716
258	32	2.4	360	5	BY136947	BY136947			C 331	31	2.3	533	6	CV7280151	CV7280151
259	32	2.4	369	2	BE331872	BE331872			C 332	31	2.3	534	6	CV7298822	CV7298822
260	32	2.4	369	2	BY136126	BY136126			C 333	31	2.3	534	6	CV7291397	CV7291397
261	32	2.4	372	5	BY773478	BY773478			C 334	31	2.3	534	6	CV7291722	CV7291722
262	32	2.4	373	10	CG499616	CG499616			C 335	31	2.3	534	6	CV7291856	CV7291856
263	32	2.4	376	5	BG241026	BG241026			C 336	31	2.3	534	6	CV7291890	CV7291890
264	32	2.4	376	5	BY772949	BY772949			C 337	31	2.3	534	6	CV7291946	CV7291946
265	32	2.4	383	3	BM690614	BM690614			C 338	31	2.3	534	6	CV7310916	CV7310916
266	32	2.4	387	5	DN845855	DN845855			C 339	31	2.3	534	6	CV7312475	CV7312475
267	32	2.4	388	8	DN845855	DN845855			C 340	31	2.3	540	3	BI516301	BI516301
268	32	2.4	391	8	DN105580	DN105580			C 341	31	2.3	542	6	CV7292046	CV7292046
269	32	2.4	398	8	DN105580	DN105580			C 342	31	2.3	542	7	CV729541	CV729541
270	32	2.4	420	1	AJ476192	AJ476192			C 343	31	2.3	546	7	CV730304	CV730304
271	32	2.4	424	1	AM212054	AM212054			C 344	31	2.3	546	6	CV7291987	CV7291987
272	32	2.4	482	1	BI551830	BI551830			C 345	31	2.3	552	6	CV7291845	CV7291845
273	32	2.4	490	6	CA702167	CA702167			C 346	31	2.3	553	6	CV7291221	CV7291221
274	32	2.4	490	6	CA702167	CA702167			C 347	31	2.3	553	6	CV7316322	CV7316322
275	32	2.4	509	5	BE553950	BE553950			C 348	31	2.3	565	6	CV7313386	CV7313386
276	32	2.4	512	2	BE553950	BE553950			C 349	31	2.3	570	6	CV7282305	CV7282305
277	32	2.4	513	6	CA236892	CA236892			C 350	31	2.3	572	6	CV7291116	CV7291116
278	32	2.4	528	8	CM601944	CM601944			C 351	31	2.3	574	6	CV7295691	CV7295691
279	32	2.4	532	8	CM601944	CM601944			C 352	31	2.3	574	6	CV7315283	CV7315283
280	32	2.4	533	7	AM680772	AM680772			C 353	31	2.3	576	6	CV7281530	CV7281530
281	32	2.4	545	7	CF964338	CF964338			C 354	31	2.3	576	6	CV7292157	CV7292157
282	32	2.4	553	3	BM526699	BM526699			C 355	31	2.3	579	6	CV729696	CV729696
283	32	2.4	570	2	BE371134	BE371134			C 356	31	2.3	579	6	CV7318970	CV7318970
284	32	2.4	615	7	CF992234	CF992234			C 357	31	2.3	579	6	CV7328416	CV7328416
285	32	2.4	644	10	CM153948	CM153948			C 358	31	2.3	580	6	CV7292290	CV7292290
286	32	2.4	655	3	BI853324	BI853324			C 359	31	2.3	580	6	CV7333546	CV7333546
287	32	2.4	658	6	CB967344	CB967344			C 360	31	2.3	582	6	CV7291777	CV7291777
288	32	2.4	708	6	CB964909	CB964909			C 361	31	2.3	582	6	CV7314730	CV7314730
289	32	2.4	708	6	CB964909	CB964909			C 362	31	2.3	583	6	CV7291068	CV7291068
290	32	2.4	709	6	CB966697	CB966697			C 363	31	2.3	583	6	CV7316852	CV7316852
291	32	2.4	709	6	CB967280	CB967280			C 364	31	2.3	584	6	CV7287876	CV7287876
292	32	2.4	713	6	CB966859	CB966859			C 365	31	2.3	585	6	CV7281885	CV7281885
293	32	2.4	762	8	DN105822	DN105822			C 366	31	2.3	585	6	CV729782	CV729782
294	32	2.4	763	3	BI646175	BI646175			C 367	31	2.3	586	6	CV7310550	CV7310550
295	32	2.4	865	3	BI953640	BI953640			C 368	31	2.3	587	6	CV7291393	CV7291393
296	32	2.4	1014	3	BO225456	BO225456			C 369	31	2.3	587	6	CV7314886	CV7314886
297	32	2.4	1014	3	BO225456	BO225456			C 370	31	2.3	588	6	CV7276491	CV7276491
298	32	2.4	129	7	CV729474	CV729474			C 371	31	2.3	588	6	CV7281739	CV7281739
299	32	2.3	144	6	CF291121	CF291121			C 372	31	2.3	588	6	CV7290881	CV7290881
300	31	2.3	283	6	CF292141	CF292141			C 373	31	2.3	589	6	CV728388	CV728388
301	31	2.3	315	7	CV732687	CV732687			C 374	31	2.3	592	6	CV7279120	CV7279120
302	31	2.3	320	1	AU101458	AU101458			C 375	31	2.3	593	2	BG050202	BG050202
303	31	2.3	343	6	CF300711	CF300711			C 376	31	2.3	593	6	CV7277948	CV7277948
304	31	2.3	370	1	AU095084	AU095084			C 377	31	2.3	593	6	CV733831	CV733831
305	31	2.3	371	8	D15463	D15463			C 378	31	2.3	600	6	CV7328581	CV7328581
306	31	2.3	393	1	AU164375	AU164375			C 379	31	2.3	602	6	CV729468	CV729468
307	31	2.3	404	7	CV731779	CV731779			C 380	31	2.3	603	6	CV7291541	CV7291541
308	31	2.3	405	10	CF966699	CF966699			C 381	31	2.3	621	6	CV729499	CV729499
309	31	2.3	410	6	CF317868	CF317868			C 382	31	2.3	621	6	CV7326829	CV7326829
310	31	2.3	412	1	AU161888	AU161888			C 383	31	2.3	630	1	AM431803	AM431803
311	31	2.3	433	6	CF294639	CF294639			C 384	31	2.3	632	3	BM374043	BM374043
312	31	2.3	435	6	DN349204	DN349204			C 385	31	2.3	659	6	CV7317769	CV7317769
313	31	2.3	448	6	CF292222	CF292222			C 386	31	2.3	664	6	CV7326822	CV7326822
314	31	2.3	454	1	AU184386	AU184386			C 387	31	2.3	673	6	CV7278180	CV7278180

C 388	31	2.3	674	6	CE293377	CE293377 30DGS--02	C 461	29	2.2	309	7	CN368930	CN368930 170004250
C 389	31	2.3	675	6	CE281691	CE281691 14ETTL--08	462	29	2.2	309	10	CG512689	CG512689 OST65712
C 390	31	2.3	697	6	CF300146	CF300146 7LEAF--04	463	29	2.2	315	1	AV948856	AV948856 AV948856
C 391	31	2.3	697	6	CF318264	CF318264 HD--08-F0	464	29	2.2	318	6	CH133093	CH133093 K-EST0210
C 392	31	2.3	744	10	CM647351	CM647351 OA_Aba018	465	29	2.2	319	10	CG671515	CG671515 OST500536
C 393	31	2.3	750	6	CP317337	CP317337 HD--06-P2	466	29	2.2	342	5	BY353066	BY353066 BY353066
C 394	31	2.3	777	6	CE291028	CE291028 14ROOF--00	467	29	2.2	344	3	BM538414	BM538414 ha95402..9
C 395	31	2.3	822	2	CK125022	CK125022 BES182411	468	29	2.2	345	6	CF531239	CF531239 UT-M-FYO-
C 396	31	2.3	835	8	CK778848	CK778848 UT-BH-HG2	469	29	2.2	345	8	DN394778	DN394778 LIB3934-0
C 397	31	2.3	871	3	BI649354	BI649354 603278090	470	29	2.2	347	10	CG549590	CG549590 OST153477
C 398	31	2.3	1054	3	BM547201	BM547201 AGENCOURT	471	29	2.2	349	3	BI818861	BI818861 603077331
C 399	31	2.3	1099	10	CM934002	CM934002 EDCCL89TF	472	29	2.2	349	5	BY382273	BY382273 BY382273
C 400	31	2.3	1761	10	CL165940	CL165940 OaIFCC040	473	29	2.2	352	5	BY217229	BY217229 BY217229
C 401	30	2.3	219	7	CN284618	CN284618 170005315	474	29	2.2	350	5	BY220368	BY220368 BY220368
C 402	30	2.3	248	3	BM096860	BM096860 EBma07_SQ	475	29	2.2	352	5	BY220368	BY220368 BY220368
C 403	30	2.3	353	6	CB661319	CB661319 OSONE03P	476	29	2.2	352	10	CG549167	CG549167 OST152040
C 404	30	2.3	455	1	AL508411	AL508411 AL508411	477	29	2.2	354	5	BY147222	BY147222 BY147222
C 405	30	2.3	465	5	BM224472	BM224472 BM224472	478	29	2.2	358	2	BB841720	BB841720 BB841720
C 406	30	2.3	515	3	BI778822	BI778822 EBRO07_SQ	479	29	2.2	360	7	CK661058	CK661058 LP20155..3
C 407	30	2.3	524	10	AV949227	AV949227 AV949227	480	29	2.2	365	1	AI119251	AI119251 u624C06..Y
C 408	30	2.3	533	10	CL152989	CL152989 104_337..1	481	29	2.2	366	1	AA615835	AA615835 u690H09..T
C 409	30	2.3	545	5	BM220946	BM220946 BM220946	482	29	2.2	366	5	BY176775	BY176775 BY176775
C 410	30	2.3	554	5	BU979754	BU979754 HI08F07r	483	29	2.2	366	10	CG651246	CG651246 OM_Ba020
C 411	30	2.3	559	8	DR002175	DR002175 TC125347	484	29	2.2	367	5	BY192028	BY192028 BY192028
C 412	30	2.3	584	5	BQ462701	BQ462701 HI01L23T	485	29	2.2	367	5	BY198390	BY198390 BY198390
C 413	30	2.3	589	1	AL503966	AL503966 AL503966	486	29	2.2	369	5	CN402626	CN402626 170006001
C 414	30	2.3	589	1	BM228224	BM228224 BM228224	487	29	2.2	371	7	CN402626	CG499617 OST41869
C 415	30	2.3	601	5	CA032801	CA032801 HX14D23r	488	29	2.2	379	10	CG499617	DN348989 LIB3578-0
C 416	30	2.3	604	5	BM224392	BM224392 BM224392	489	29	2.2	382	5	BY772109	BY772109 BY772109
C 417	30	2.3	604	7	CK123752	CK123752 BES182410	490	29	2.2	387	2	BF425160	BF425160 BU54160 8u54D11..Y
C 418	30	2.3	608	5	BM2230484	BM2230484 BM2230484	491	29	2.2	392	1	AA792353	AA792353 v691F07..T
C 419	30	2.3	632	5	BM223898	BM223898 BM223898	492	29	2.2	393	5	BM223990	BM223990 BM223990
C 420	30	2.3	633	1	AV913160	AV913160 AV913160	493	29	2.2	398	7	CK073626	CN366942 170005318
C 421	30	2.3	637	1	BM227587	BM227587 AV985941	494	29	2.2	402	7	CK073626	CK073626 71554861C
C 422	30	2.3	639	1	AV985941	AV985941 AV985941	495	29	2.2	403	6	CF722779	CF722779 B07-LKFOC
C 423	30	2.3	643	5	BM227210	BM227210 BM227210	496	29	2.2	406	5	BU981288	BU981288 HA23C20r
C 424	30	2.3	644	5	BU998606	BU998606 H111J16r	497	29	2.2	406	8	DN389076	DN389076 LIB3895-0
C 425	30	2.3	645	5	BM226199	BM226199 BM226199	498	29	2.2	407	2	BE457585	BE457585 u693D12..X
C 426	30	2.3	646	7	CN982817	CN982817 51361..126	499	29	2.2	414	1	AI752180	AI752180 cml4D08..Y
C 427	30	2.3	649	5	BM223538	BM223538 BM223538	500	29	2.2	414	3	BQ133789	BQ133789 sanelD01..
C 428	30	2.3	655	5	BU995179	BU995179 HM09H10r							
C 429	30	2.3	655	5	BM032024	BM032024 BM032024							
C 430	30	2.3	660	5	BM239205	BM239205 BM239205							
C 431	30	2.3	664	5	BM231584	BM231584 BM231584							
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C 433	30	2.3	666	5	BM103786	BM103786 BM103786							
C 434	30	2.3	667	6	CB660414	CB660414 OSUNE02B							
C 435	30	2.3	677	10	CM153947	CM153947 104_555..1							
C 436	30	2.3	684	5	BM239283	BM239283 BM239283							
C 437	30	2.3	685	9	AZ261292	AZ261292 1M0104K21							
C 438	30	2.3	685	10	CM493507	CM493507 ISBD001F2							
C 439	30	2.3	694	5	BM225031	BM225031 BM225031							
C 440	30	2.3	703	6	BM230303	BM230303 BM230303							
C 441	30	2.3	709	6	CB966798	CB966798 NL43_A05							
C 442	30	2.3	715	2	BEA13366	BEA13366 MCG011_H1							
C 443	30	2.3	718	5	BM222596	BM222596 BM222596							
C 444	30	2.3	718	5	BM226615	BM226615 BM226615							
C 445	30	2.3	719	5	BM227955	BM227955 BM227955							
C 446	30	2.3	726	10	CM276703	CM276703 104_750..1							
C 447	30	2.3	726	5	BM222468	BM222468 BM222468							
C 448	30	2.3	726	10	CM870869	CM870869 she2h9-9							
C 449	30	2.3	743	8	DR006933	DR006933 TC116427							
C 450	30	2.3	754	10	CG286322	CG286322 OC_Ba025							
C 451	30	2.3	761	10	CG271371	CG271371 OC_Ba006							
C 452	30	2.3	987	2	BF942686	BF942686 SC18_CDNA							
C 453	30	2.3	1004	6	CB575709	CB575709 AGENCOURT							
C 454	29	2.2	202	7	CN368931	CN368931 170005312							
C 455	29	2.2	245	3	BP433279	BP433279 BP433279							
C 456	29	2.2	246	3	BM441534	BM441534 EBma05_SQ							
C 457	29	2.2	260	10	CM173942	CM173942 104_585..1							
C 458	29	2.2	284	8	DN375873	DN375873 LIB38529							
C 459	29	2.2	290	7	CN368939	CN368939 170005311							
C 460	29	2.2	301	7	CK060191	CK060191 63024r51c							

ALIGNMENTS

RESULT 1
LOCUS
DEFINITION
Cot 10-normalized of Homo sapiens (human).

ACCESSION
C612083.1 GI:50492890
VERSION
C612083.1
KEYWORDS
HTC; CNSLT; CDNA.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

REFERENCE
1 (bases 1 to 901)
Li, W.-B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
unpublished

REFERENCE
Contact: Peng Liang Email: filiang@life.techn.com URL:
http://fulllength.invtiogen.com/Invitrogen Corporation 1600
Paradise Avenue
2 (bases 1 to 901)

REFERENCE
Submitted (20-UTL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry Cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES
source
Location/Qualifiers
1..901
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D015F12"
/tissue_type="T cells (Jurkat cell line) Cot
10-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 56.1%; Score 741; DB 4; Length 901;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 741; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 581 GTGATCACTGCTCCCTGAGCACTCAAGCTGTGTGACGGTCCCTCATCAGCCGAC 640
DB 1 GTGATCACTGCTCCCTGAGCACTCAAGCTGTGTGACGGTCCCTCATCAGCCGAC 60
OY 641 AGCCAGGGGCGGAGAGAGATGCTGTCTCAGAGGATGCTGTGCGCTCCGAG 700
DB 61 AGCCAGGGGCGGAGAGAGATGCTGTCTCAGAGGATGCTGTGCGCTCCGAG 120
OY 701 AGCAAGTGTCAAGCAAGCAAGTCCAGAGCGGAGTCTAGCCCGCGCTCGCCAC 760
DB 121 AGCAAGTGTCAAGCAAGCAAGTCCAGAGCGGAGTCTAGCCCGCGCTCGCCAC 180
OY 761 GACCGCTGCGCGCTGCGCGCTGCGCGCGGAGCGCTTCCACCGCTTCCACCGC 820
DB 181 GACCGCTGCGCGCTGCGCGCTGCGCGCGGAGCGCTTCCACCGCTTCCACCGC 240
OY 821 TATCCGTAAGTCAAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 880
DB 241 TATCCGTAAGTCAAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 300
OY 881 GAGCGCCCACTCAAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 940
DB 301 GAGCGCCCACTCAAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 360
OY 941 GAATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1000
DB 361 GAATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 420
OY 1001 ATGATAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1060
DB 421 ATGATAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 480
OY 1061 AGTGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1120
DB 481 AGTGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 540
OY 1121 GAGCACTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1180
DB 541 GAGCACTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 600
OY 1181 GAGGGGAGCGGCTCAAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1240
DB 601 GAGGGGAGCGGCTCAAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 660
OY 1241 AAAGAGAGATCAAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1300
DB 661 AAAGAGAGATCAAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 720
OY 1301 GCTGCTAGAGTCAAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1360
DB 721 GCTGCTAGAGTCAAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 780

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RESULT 2
BM922276

LOCUS BM922276 1046 bp mRNA linear EST 12-MAR-2002
DEFINITION AGENCOUNT_6707077 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5754437
5', mRNA sequence.
ACCESSION BM922276
VERSION BM922276.1 GI:19372655
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1046)
NIH-MGC <http://imgc.ncbi.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
TITLE Email: CGAP@f-mail.nih.gov
COMMENT Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
<http://image.lnl.gov>
Plate: L14M12791 row: n column: 06
High quality sequence stop: 671.

FEATURES
source
Location/Qualifiers
1..1046
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5754437"
/lab_host="DH10B"
/clone_lib="NIH_MGC_115"

/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is inserted upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 47.8%; Score 632; DB 3; Length 1046;
Best Local Similarity 99.7%; Pred. No. 4.2e-300;
Matches 732; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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OY 347 CCGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 406
DB 1 CCGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60
OY 407 CCGTCAATGACCGCTTATGAGGGGGTCAACAGACCGCGCGCGCGCGCGCGCGCG 466
DB 61 CCGTCAATGACCGCTTATGAGGGGGTCAACAGACCGCGCGCGCGCGCGCGCGCG 120
OY 467 AATGTCTCTGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 526
DB 121 AATGTCTCTGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 180
OY 527 CTGAGATTGTTCAGATCATCATGTGTGTGTATATGTGTGTGTGTGTGTGTATC 586
DB 181 CTGAGATTGTTCAGATCATCATGTGTGTGTGTATATGTGTGTGTGTGTGTGTATC 240
OY 587 ACGGCGCTGAGCGCACTAAGAGTGTGCAAGCGGTCTTCAATCAGCGCGCACGCG 646
DB 241 ACGGCGCTGAGCGCACTAAGAGTGTGCAAGCGGTCTTCAATCAGCGCGCACGCG 300
OY 647 GGGCGAGAGAGAGAGATGCTGTCTCTCAGAGATGCTGTGCGCTTGTGAGAGACA 706
DB 301 GGGCGAGAGAGAGAGATGCTGTCTCTCAGAGATGCTGTGCGCTTGTGAGAGACA 360

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Qy	707	GTGTACGGCAACGGAATCCCAAGCCGAGGCTTACCGCCCGCTCGGCGCACGACCGC	766
Db	361	GTGTACGGCAACGGAATCCCAAGCCGAGGCTTACCGCCCGCTCGGCGCACGACCGC	420
Qy	767	CTGGCCGTGCGCCCTTGCGCCAGCGGAGCGCTTCAACCGCTTCAAGCCACTATATCG	826
Db	421	CTGGCCGTGCGCCCTTGCGCCAGCGGAGCGCTTCAACCGCTTCAAGCCACTATATCG	480
Qy	827	TACCTGCAAGACGAGATGAGCCTGCGACCCACATCTGCTGTGAGCGGGAGAGAGCC	886
Db	481	TACCTGCAAGACGAGATGAGCCTGCGCCACATCTGCTGTGAGCGGGAGAGAGCC	540
Qy	887	CCACCCTTACAGAGGCCCTGTGACCTCTCAGCTTGGGAGCCCGAGCAGCTGGAACTG	946
Db	541	CCACCCTTACAGAGGCCCTGTGACCTCTCAGCTTGGGAGCCCGAGCAGCTGGAACTG	600
Qy	947	AACCGGAGTGGTGGCGGCGCACCCGCCAAACAGAACCATCTTTCAGACGTGACTGATG	1006
Db	601	AACCGGAGTGGTGGCGGCGCACCCGCCAAACAGAACCATCTTTCAGACGTGATGAT	660
Qy	1007	AGTGCAGGCTGGGCGGCCCTCTGCCCCCGACGATTAATCTGGGGATACAGCGCCACGTGC	1066
Db	661	AGTGCAGGCTGGGCGGAGCCCTGCCCCCGACGATTAATCTGGGGATACAGCGCCACGTGC	720
Qy	1067	TACGCGAGCGGCGG 1080	
Db	721	TACGCGAGCGGCGG 734	

RESULT 3
B0641849
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

B0641849 967 bp mRNA linear EST 15-JUL-2002
AGENCOURT 8287174 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:6292265
5', mRNA sequence.
B0641849
B0641849.1 GI:21766021
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 967)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgasbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ULNL at:
<http://image.llnl.gov>
Plate: L16CM2493 row: g column: 18
High quality sequence drop: 571.

FEATURES
source

```

1..967
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6292265"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/clone_lib="M13 MGC 43"
/note="Organ: eye; Vector: pOT8; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GCCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit

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ORIGIN
      (Stratagene) and Superscript II RT (Life Technologies) .
      Note: this is a NIH_MGC Library.  |
Query Match      46.5%;   Score 614;   DB 5;   Length 967;
Best Local Similarity 99.7%;   Pred. No. 3,28-291;
Matches 714;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0.

```

[illegible]

RESULT 4
DN992322
LOCUS
DEFINITION
DN992322 647 bp mRNA linear EST 17-MAY-2005
TC124411 Human adult whole brain, large insert, PCMV expression
library, Homo sapiens cDNA clone TC124411 5' similar to Homo sapiens
transmembrane, prostrate androgen induced RNA (TMEDAI), transcript
variant 4, mRNA sequence.
ACCESSION
DN992322
VERSION
DN992322.1 GI:66252153
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
1 (bases 1 to 647)
REFERENCE

Db 541 CTCCTTCTCTGAGGGGACCCCGGCTCCACCAACACATCCGGCCCCCTAGAGAGCGGAGC 6000

QY 1231 CATCTGGAG 1239

Db 601 CATCTGGAG 609

LOCUS	DEFINITION	551 bp	mRNA	linear	EST	12-MAR-2007
BM141979	1f55a11.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens cDNA clone IMAGE:5677341 5' similar to TR:Q9UUD3 Q9UUD3 D7718J7.1					
LOCUS	DEFINITION	551 bp	mRNA	linear	EST	12-MAR-2007
BM141979	1f55a11.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens cDNA clone IMAGE:5677341 5' similar to TR:Q9UUD3 Q9UUD3 D7718J7.1					
LOCUS	DEFINITION	551 bp	mRNA	linear	EST	12-MAR-2007
BM141979	1f55a11.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens cDNA clone IMAGE:5677341 5' similar to TR:Q9UUD3 Q9UUD3 D7718J7.1					

ACCESSION	BM141979	GI:17152046
VERSION	BM141979.1	
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

FEATURES
source

ORIGIN

Query Match	41.6%;	Score 550;	DB 3;	Length 551;
Best Local Similarity	100.0%;	Pred. No. 1.2e-259;		
Matches 550;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

OY	714	GCAACGGAAATCCCAAGACCGCGAAGGTCTAACGCCCGCTCGGAGCCACAGACCGCTGCACG	773
Db	1	GCAACGGAAATCCCAAGACCGCGAAGGTCTAACGCCCGCTCGGAGCCACAGACCGCTGCACG	60
OY	774	TGCCGCCCTTCGACCAGCGGAGAGCGCTTCACACGCTTTCAGGCCCACTATCCGTAACCTGC	833
Db	61	TGCCGCCCTTCGACCAGCGGAGAGGCTTCCACCGCTTTCAGGCCCACTATCCGTAACCTGC	120
OY	834	AGCAGCGAATCGACCTTGCAACCCACCAATCTCGCTGTCAAGACGGGGAGAGGCCCCCACTCT	893
Db	121	AGCAGCGAATCGACCTTGCAACCCACCACTCTCGCTGTCAAGACGGGGAGAGGCCCCCACTCT	180
OY	894	ACGAGGAGCCCTGCACCTCGAGCTTGAGGAGCCCGAGCAGACCTGGAATCGAAACGGG	953
Db	181	ACGAGGAGCCCTGCACCTCTCACTTTGGAGACCCCGAGCAGACCTGGAATCGAAACGGG	240
OY	954	AGTGGATGCGCGACCCCAAGAAACAATCTTTCAGACGTGACCTGATGATAGTCCA	1013
Db	241	AGTGGATGCGCGACCCCAAGAAACAATCTTTCAGACGTGACCTGATGATAGTCCA	300
OY	1014	GGCTGGGCGGCGCTTCGCCCCCAGCAGTAACTTGCGCATTCAGGCGCACTGTGCTAACGGCA	1073
Db	301	GGCTGGGCGGCGCTTCGCCCCCAGCAGTAACTTGCGCATTCAGGCGCACTGTGCTAACGGCA	360
OY	1074	GCGGCGGCGCGATGGAAGGAGGCGCGCGCCACCTACAGCAGAGGTATCGGCGCACTACCGG	1133
Db	361	GCGGCGGCGCGATGGAAGGAGGCGCGCGCCACCTACAGCAGAGGTATCGGCGCACTACCGG	420
OY	1134	GATCTCTCTTCAGACACAGCAGAGCAGTGGGCGCGCTCTCTTGCTGGAAGGAGCCCGGC	1193
Db	421	GATCTCTCTTCAGACACAGCAGAGCAGTGGGCGCGCTCTCTTGCTGGAAGGAGCCCGGC	480
OY	1194	TTCACCAACAACAATGCGCGCTTAAAGAGCGCACTGTGAGCGAAGAAGAGATA	1253
Db	481	TTCACCAACAACAATGCGCGCTTAAAGAGCGCACTGTGAGCGAAGAAGAGATA	540
OY	1254	AACGAAAGG 1263	
Db	541	AACGAAAGG 550	

RESULT 8	
DN991959	
LOCUS	601 bp mRNA linear EST 17-MAY-2005
DEFINITION	TC13J306 Human adult whole brain, large insert, cDNA expression library Homo sapiens cDNA clone TC13J306 5' similar to Homo sapiens transmembrane, prostate androgen induced RNA (TMEMPA1), transcript variant 1, mRNA sequence.
ACCESSION	DN991959
VERSION	DN991959.1
KEYWORDS	GI:66251790
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	1 (bases 1 to 601)
AUTHORS	Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L., Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M., Zhang,X., Jay,G., and He,W.
TITLE	High-throughput cloning of full-length human cDNAs directly from cDNA libraries optimized for large and rare transcripts
JOURNAL	Unpublished (2005)
COMMENT	Contact: Kovacs, KF High Throughput cDNA Cloning Origene Technologies, Inc. (www.origene.com) 6 Taft Court, Suite 100, Rockville, MD 20850, USA Tel: 301 340 3188 Fax: 301 340 8606


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QY 670 GTCTTCAAGAGATGCTGTGGCCCTGGAGAGCAAGTGTGAGGCAACGGAATCCGCA 729
DB 1 GTCTTCAAGAGATGCTGTGGCCCTGGAGAGCAAGTGTGAGGCAACGGAATCCGCA 60
QY 730 GCCGAGGTCTAAGCGCCCGCTGGCCCAAGCAAGCGCTGGCCGCTTCCGCA 789
DB 61 GCCGAGGTCTAAGCGCCCGCTGGCCCAAGCAAGCGCTGGCCGCTTCCGCA 120
QY 790 GCGGAGGCTTCCAGCGCTTCCAGCGCACTTATCCGTAAGCAAGATGACCT 849
DB 121 GCGGAGGCTTCCAGCGCTTCCAGCGCACTTATCCGTAAGCAAGATGACCT 180
QY 850 GCCACCCATCTCTGTGTGAGAGGAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAG 909
DB 181 GCGGAGGCTTCCAGCGCTTCCAGCGCACTTATCCGTAAGCAAGATGACCT 240
QY 910 CCTCAGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 969
DB 241 CCTCAGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 970 CCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1029
DB 301 CCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 1030 CCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1089
DB 361 CCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 1090 GCGGAGGCTTCCAGCGCTTCCAGCGCACTTATCCGTAAGCAAGATGACCT 1149
DB 421 GCGGAGGCTTCCAGCGCTTCCAGCGCACTTATCCGTAAGCAAGATGACCT 480
QY 1150 CCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1194
DB 481 CCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 525

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RESULT 16
BUS27705 1068 bp mRNA linear EST 13-SEP-2002
LOCUS AGNCOURT_10186171 NIH_MGC_101 Homo sapiens cDNA clone
DEFINITION IMAGE:5537543 5', mRNA sequence.
ACCESSION BUS27705.1 GI:22838146
VERSION BUS27705.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 1068)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L16M2700 row: k column: 15
High quality sequence stop: 468.
Location/Qualifiers
1..1068
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5537543"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"

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/clone 11b="NIH_MGC_101"
/notes="Organ: lung; Vector: pOTB7; Site 1: EcoRI; Site 2:
XhoI; cDNA made by oligo-dt priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGAGCAGAG (G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC library."

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Query Match 35.7%; Score 471; DB 5; Length 1068;
Best Local Similarity 100.0%; Pred. No. 1,1e-220;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 92 GGGAAAGCTAGCGGCAAGAGCTAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 151
DB 21 GGGAAAGCTAGCGGCAAGAGCTAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 80
QY 152 TTTCGGAGCGCACCGCGGCGGCACTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 211
DB 81 TTTCGGAGCGCACCGCGGCGGCACTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 140
QY 212 GGGGCGGAGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 271
DB 141 GGGGCGGAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 200
QY 272 CGAGCCGAGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 331
DB 201 CGAGCCGAGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 260
QY 332 CCGGAGCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 391
DB 261 CCGGAGCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 320
QY 392 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 451
DB 321 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 380
QY 452 GCGCGCGGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 511
DB 381 GCGCGCGGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 440
QY 512 ATGAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 562
DB 441 ATGAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 491

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RESULT 17
B0691705 655 bp mRNA linear EST 15-JUL-2002
LOCUS AGNCOURT_8046876 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6208935
DEFINITION 5', mRNA sequence.
ACCESSION B0691705
VERSION B0691705.1 GI:21817021
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 655)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

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LOCUS	AV419334	780 bp	DNA	linear	GSS 17-DEC-2003
DEFINITION	Homo sapiens TM6P1 gene, VIRTUAL TRANSCRIPT, partial sequence,				
ACCESSION	AV419334				
VERSION	AV419334.1 GI:39775291				
KEYWORDS	GSS.				
ORGANISM	Homo sapiens (human)				
REFERENCE	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.				
AUTHORS	1 (bases 1 to 780) Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tenebaum,D.M., Ciavella,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 780)				
AUTHORS	Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tenebaum,D.M., Ciavella,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	These sequences were made by sequencing genomic exons and ordering them based on alignment.				
FEATURES	Location/Qualifiers				
source	1..780				
gene	/organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" <1..>780 /gene="TM6P1" /locus_tag="HCM6856"				
ORIGIN					
Query Match	33.5%	Score 442;	DB 10;	Length 780;	
Best Local Similarity	100.0%	Pred. No. 2.3e-206;			
Matches	442;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	835	GACGAGATCGA	CTTGCCACCA	CCATCTCGCTGTCA	GCGGAGAGAGACCCCCACCTTA 894
DB	339	GCACGAGATCGA	CTGCCACCA	CCATCTCGCTGTCA	GCGGAGAGAGACCCCCACCTTA 398
QY	895	CCAGGGCCCCCTG	CACCTTCAGCTT	TGGGAGACCCCGAGCA	CGCTGGAATGAACCGGGA 954
DB	399	CCAGGGCCCCCTG	CACCTTCAGCTT	TGGGAGACCCCGAGCA	CGCTGGAATGAACCGGGA 458
QY	955	GTCCGGGCGGCA	CCCCCAAGAAC	CACTCTTCAGAC	GTGACCTGATGATAGTCCAG 1011
DB	459	GTCCGGGCGGCA	CCCCCAAGAAC	CACTCTTCAGAC	GTGACCTGATGATAGTCCAG 518
QY	1015	GCTGGGCGGCCC	CTGCCCCCAGCA	GTAACTTGGGCAT	CAGCGCCACGTGCTACGCGCAG 107
DB	519	GCTGGGCGGCCC	CTGCCCCCAGCA	GTAACTTGGGCAT	CAGCGCCACGTGCTACGCGCAG 578
QY	1075	CGGCGGGCGCAT	TGAGAGGGG	CGCGCCGCA	CTTACGCGGAGTATGCGGCACCTA 113
DB	579	CGGCGGGCGCAT	TGAGAGGGG	CGCGCCGCA	CTTACGCGGAGTATGCGGCACCTA 638
QY	1135	GTCTCTCTTC	CACGACGAG	ACAGTGGG	CGCCCTCTTGTGAGAGGAGACCCGGCT 119
DB	639	GTCTCTCTTC	CACGACGAG	ACAGTGGG	CGCCCTCTTGTGAGAGGAGACCCGGCT 698
QY	1195	CCACCA	CACACATCG	CGCCCTTAGAG	ACGCGCATCTTGAGCAAAAGAGATTA 125
DB	699	CCACCA	CACACATCG	CGCCCTTAGAG	ACGCGCATCTTGAGCAAAAGAGATTA 758
QY	1255	ACGAAA	AGCACCCTCT	CTCTAG	1276

```

Db          759 ACAGAAAGGACCCCTCTCTAG 780
|||||
RESULT 23
BM712680
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
PUBMED

BM712680 461 bp mRNA linear EST 28-FEB-2002
UI-E-EJ0-abg-a-10-0-UI.r1 UI-E-EJ0 Homo sapiens cDNA clone
UI-E-EJ0-abg-a-10-0-UI 5', mRNA sequence.
BM712680
BM712680.1 GI:19025938
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 461)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
8889548
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: Bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.regen.com).
Seq primer: M13 Reverse.
Location/Qualifiers
1. 461
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-EJ0-abg-a-10-0-UI"
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
/dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_1ib="UI-E-EJ0"
/notes="Organ: eye; Vector: pTT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-EJ0 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pTT73-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes,
AGACTACAGA; lens, CGATTAGCGA; eye anterior segment,
AATGCCGAT; optic nerve, CCAATAGAG; retina, CCGCG; Retina
Foveal and Macular, CTCG; RPE and Choroid, ACCTA. This
library was created for the program, Gene Discovery in the
Visual System, supported by National Eye Institute (NEI).

```



```
Db 1 GAGCCCCCACTTACAGAGGCCCCCTTGACCTTCCAGCTTCGGAGACCCCGAGCAGCAGCTG 60
Qy 941 GAACGTAAACCGGAGTGGTGGTGGCGGACCCCAACAGAACCATCTTGACAGTACCTG 1000
Db 61 GAACGTAAACCGGAGTGGTGGTGGCGGACCCCAACAGAACCATCTTGACAGTACCTG 120
Qy 1001 ATGATTAATGCAAGGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1060
Db 121 ATGATTAATGCAAGGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 180
Qy 1061 ACGTCTACAGGCGAGGCGGCGGCGATGAGAGGAGGCGCGCCGACCTTACAGAGGATCATC 1120
Db 181 ACGTCTACAGGCGAGGCGGCGGCGATGAGAGGAGGCGCGCCGACCTTACAGAGGATCATC 240
Qy 1121 GGGCACTACCGCGGGGTCTCTCTTCCAGACAGCAGAGCAGTGGCGCGCTCTTGGTG 1180
Db 241 GGGCACTACCGCGGGGTCTCTCTTCCAGACAGCAGAGCAGTGGCGCGCTCTTGGTG 300
Qy 1181 GAGGAGGAGCCGGGCTTCCACACACACACATCGCGCCCTTGAAGAGGCGACATCTGAGC 1240
Db 301 GAGGAGGAGCCGGGCTTCCACACACACACATCGCGCCCTTGAAGAGGCGACATCTGAGC 360
Qy 1241 AAAGAGAGATTAACAGAAAGACACCCCTCTCTAGGGTCCCGAGGAGGCGCGGCTGGG 1300
Db 361 AAAGAGAGATTAACAGAAAGACACCCCTCTCTAGGGTCCCGAGGAGGCGCGGCTGGG 420
Qy 1301 GCTGCTAGTGAAGAGGCGAG 1321
Db 421 GCTGCTAGTGAAGAGGCGAG 441
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RESULT 24
LOCUS BM714472 633 bp mRNA linear EST 28-FEB-2002
DEFINITION UI-E-E10-shs-f-20-0-UI.r1 UI-E-E10 Homo sapiens cDNA clone
VERSION BM714472.1 GI:19027730
KEYWORDS EST.
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ACCESSION BM714472.1 GI:19027730
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
```

```
REFERENCE 1 (bases 1 to 633)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
```

```
JOURNAL Genome Res. 6 (9), 791-806 (1996)
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
```

```
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Genetics (www.reagen.com).
The following repetitive elements were found in this cDNA
sequence: 593-614, >AT rich#Low_complexity (matched complement)
Seq primer: M13 Reverse
```

```
FEATURES
SOURCE Location/Qualifiers
```

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1..633
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-E10-shs-f-20-0-UI"
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ORIGIN

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Query Match 33.1%; Score 437; DB 3; Length 633;
Best Local Similarity 100.0%; Pred. No. 6,8e-204;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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/tissue type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and Choroid"
/dev stage="Fetal and adult"
/lab host="DH10B (Life Technologies) (T1 phage resistant)"
/clone lib="UI-E-E10"
/note="Organ: eye; Vector: pRTT3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-E10 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pRTT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (drr)18 tail. The sequence tags for this library are: fetal eyes, AGATCAAGA; lens, CGATTAGGA; eye anterior segment, AATGCCGAGT; optic nerve, CCATTAGTG; retina, CCGGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACTCA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

```
Qy 885 CCCCACTTACAGAGGCCCCCTTGACCTTCCAGCTTCGGAGACCCCGAGCAGCAGCTGAGC 944
Db 14 CCCCACTTACAGAGGCCCCCTTGACCTTCCAGCTTCGGAGACCCCGAGCAGCAGCTGAGC 73
Qy 945 TGAACCGGAGTGGTGGTGGCGGACCCCAACAGAACCATCTTGACAGTACCTGATGG 1004
Db 74 TGAACCGGAGTGGTGGTGGCGGACCCCAACAGAACCATCTTGACAGTACCTGATGG 133
Qy 1005 ATATGTCAGAGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1064
Db 134 ATATGTCAGAGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 193
Qy 1065 GCTACGCGCAGCGGGGCGGATGAGAGGAGGCGCGCCCACTTACAGAGGATCATCGGCC 1124
Db 194 GCTACGCGCAGCGGGGCGGATGAGAGGAGGCGCGCCCACTTACAGAGGATCATCGGCC 253
Qy 1125 ACTACCGGGGCTCTCTTCCAGACACAGACAGCAGTGGCGCGCTCTTGGTGAGG 1184
Db 254 ACTACCGGGGCTCTCTTCCAGACACAGACAGCAGTGGCGCGCTCTTGGTGAGG 313
Qy 1185 GAGCCGGGCTCCACACACACATGCGGCGCCCTTGAAGAGCGGACATGAGCAAG 1244
Db 314 GAGCCGGGCTCCACACACACATGCGGCGCCCTTGAAGAGCGGACATGAGCAAG 373
Qy 1245 AGAAGATTAACAGAAAGACACCTCTTGAAGGTCCCGAGGAGGCGCGGCTGGGGCTG 1304
Db 374 AGAAGATTAACAGAAAGACACCTCTTGAAGGTCCCGAGGAGGCGCGGCTGGGGCTG 433
Qy 1305 GGTAGGTGAAGAGGCGAG 1321
Db 434 GGTAGGTGAAGAGGCGAG 450
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RESULT 25
B0624784/c 588 bp mRNA linear EST 23-SEP-2002
LOCUS UI-H-FG1-bgi-f-22-0-UI.s1 NCI CGAP FG1 Homo sapiens cDNA clone
DEFINITION UI-H-FG1-bgi-f-22-0-UI 3', mRNA sequence.
ACCESSION B0624784
VERSION B0624784.1 GI:23290999
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 588)
 NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS
 TITLE
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)

JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: James Martin
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@iowa.edu
 Seq primer: M13 FORWARD
 POLYA=Yes

FEATURES
 source
 location/Qualifiers

1. 588
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-FGI-Bgl-f-22-0-UI"
 /tissue_type="Cell lines"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI-CCAP FGI"
 /note="Organ: Enchondroma; Vector: pT73-Pac (Pharmacia)
 with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
 NCI CGAP FGI is a normalized cDNA library obtained from a
 pool of mRNA from 2 cell lines from Enchondroma tissues.
 The library was constructed according to Bonaldi, Lennon
 and Soares, Genome Research, 6:791-806, 1996. First strand
 cDNA synthesis was primed with an oligo-dT primer
 containing a Not I site. Double stranded cDNA was ligated
 to an EcoR I adaptor, digested with Not I, and cloned
 directionally into pT73-Pac vector. The oligonucleotide
 used to prime the synthesis of first-strand cDNA contains
 a library tag sequence that is located between the Not I
 site and the (dT)18 tail. The sequence tag for this
 library is CGTCACTC. The cell lines were provided by Dr.
 James Martin from the University of Iowa.
 TAG_TISSUE=Enchondroma cell line (Mix of EN1 and EN2)
 TAG_LIB=UI-H-FGI
 TAG_SEQ=CGTCACTC"

ORIGIN

Query Match 32.4%; Score 428; DB 5; Length 588;
 Best Local Similarity 100.0%; Pred. No. 1.9e-199;
 Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

894 ACCAGGAGCCCTGACCTTCAGCTTCGGGACCCCGAGAGAGAGTGAACCGG 953
 588 ACCAGGAGCCCTGACCTTCAGCTTCGGGACCCCGAGAGAGAGTGAACCGG 529
 954 AGTCGGTGGCGACACCCCAACAGAACCATCTTCAGAGTGAAGTATGTCGA 1013
 528 AGTCGGTGGCGACACCCCAACAGAACCATCTTCAGAGTGAAGTATGTCGA 469
 1014 GGTGG 1073
 468 GGTGG 409
 1074 GGTGG 1133
 408 GGTGG 349
 1134 GGTGG 1193
 348 GGTGG 289
 1194 TCCACACACACACATCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1253

Db 288 TCCACACACACACATCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 229
 Qy 1254 AACGAGAGAGACCCCTCTAGGGTCCCGAGGGGGGGGGGGGGGGGGGGGG 1313
 Db 228 AACGAGAGAGACCCCTCTAGGGTCCCGAGGGGGGGGGGGGGGGGGGG 169
 Qy 1314 AAAGCAG 1321
 Db 168 AAAGCAG 161

RESULT 26
 AL558882
 LOCUS
 DEFINITION
 AL558882 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
 Homo sapiens cDNA clone CS0D015YF12 5-PRIME, mRNA sequence.
 ACCESSION
 AL558882
 VERSION
 AL558882.3 GI:46184269
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)

ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 897)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On Feb 15, 2001 this sequence version replaced gi:31283015.
 CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Email: secre@genoscope.cns.fr, Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 9945.1
 For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna/8=CS0D015D060P1&c=9945.r>.

FEATURES
 source
 location/Qualifiers

1. 897
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D015YF12"
 /cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
 /clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
 10-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 32.2%; Score 425; DB 1; Length 897;
 Best Local Similarity 99.5%; Pred. No. 5.6e-198;
 Matches 645; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

581 GTGATCAGTCTGCTGAGCAGTCAAGCTGTGAGAGGAGTGTGAGTGTGAG 640
 1 GTGATCAGTCTGCTGAGCAGTCAAGCTGTGAGAGGAGTGTGAGTGTGAG 60
 641 AGCCAGGGGGAGAGAGAGATGCTGTCTCAGAGAGATGCTGTGAGTGTGAG 700
 61 AGCCAGGGGGAGAGAGAGATGCTGTCTCAGAGAGATGCTGTGAGTGTGAG 120
 701 AGCAGGTGTCAGAGCAGATCCAGAGGCGGAGGTCTACGCCCGCTCGGACC 760
 121 AGCAGGTGTCAGAGCAGATCCAGAGGCGGAGGTCTACGCCCGCTCGGACC 179

QY 761 GACCGCTGCGCGGCGCCCTTGCCAGGAGGAGGCTTCCACCGCTTCCAGCCACC 820
 DB 180 GACCGCTGCGCGGCGCCCTTGCCAGGAGGAGGCTTCCACCGCTTCCAGCCACC 239
 QY 821 TATCCGTACTGACGACGAGATGACCTGCGACCCACCATCTGCTGTGAGCGGGAG 880
 DB 240 TATCCGTACTGACGACGAGATGACCTGCGCGCCACCATCTGCTGTGAGCGGGAG 299
 QY 881 GAGCCCCACCTTACGAGGCGCCCTGCACTCCAGCTTGGGAGCCCGGAGCAGCTG 940
 DB 300 GAGCCCCACCTTACGAGGCGCCCTGCACTCCAGCTTGGGAGCCCGGAGCAGCTG 359
 QY 941 GAACGAAACCGGAGTGGGTGGGCGACCCCAAGAACCATCTTGAAGTACCTG 1000
 DB 360 GAACGAAACCGGAGTGGGTGGGCGACCCCAAGAACCATCTTGAAGTACCTG 419
 QY 1001 ATGATAGTGCAGGCTGGGCGCCCTGCGCCCGCCAGCAGTAACTCGGAGTACGCGCC 1060
 DB 420 ATGATAGTGCAGGCTGGGCGCCCTGCGCCCGCCAGCAGTAACTCGGAGTACGCGCC 479
 QY 1061 ACGTCTACGCGCAGCGGCGGCGCATGGAGGAGGCGCCCGCCACCTACAGCGAGTATC 1120
 DB 480 ACGTCTACGCGCAGCGGCGGCGCATGGAGGAGGCGCCCGCCACCTACAGCGAGTATC 539
 QY 1121 GCGCACTACCGCGGCTCTCTCTTCCAGACGAGACGAGTGGCGCGCTCTGCTG 1180
 DB 540 GCGCACTACCGCGGCTCTCTCTTCCAGACGAGACGAGTGGCGCGCTCTGCTG 599
 QY 1181 GAGGGAGCCCGGCTCCACACACACATCGCGCCCTAGAGAGGCA 1228
 DB 600 GAGGGAGCCCGGCTCCACACACACATCGCGCCCTAGAGAGGCA 647

RESULT 27 1038 bp mRNA linear EST 23-MAR-2004
 AL517150/c Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
 LOCUS CSDDA008Y23 3-PRIME, mRNA sequence.
 DEFINITION AL517150
 ACCESSION AL517150
 VERSION AL517150.3 GI:45653717
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1038)
 TITLE Li W.B., Gruber C., Jessee J. and Polayes D.
 JOURNAL Mammalia; Euthera; Euarhontoglires; Primates; Catarrhini;
 COMMENT Unpublished (2001)
 On Feb 13, 2001 this sequence version replaced gi:30492472.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with NotI and cloned
 into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.

FEATURES
 source This sequence belongs to sequence cluster 9945.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?e=CSDDA008CA12NP1&c=9945.r.
 Location/Qualifiers
 1..1038
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSDDA008Y23"
 /tissue_type="NEUROBLASTOMA"
 /clone_lib="Homo sapiens NEUROBLASTOMA"
 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
 with a NotI-oligo(dT) primer. Five prime end enriched,"

double-strand cDNA was digested with NotI and cloned into
 the NotI and EcoRV sites of the pCMVSPORT 6 vector.
 Library was not normalized."

Query Match 32.1%; Score 424; DB 1; Length 1038;
 Best Local Similarity 99.4%; Pred. No. 1, 7e-197;
 Matches 694; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

ORIGIN
 QY 499 TTTGTTCCAGAGCATGAGATCAACGAGCTGAGAGTTTGTTCATATCATATCTGTGT 558
 DB 938 TTTGTTCCAGAGCATGAGATCAACGAGCTGAGAGTTTGTTCATATCATATCTGTGT 879
 QY 559 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 618
 DB 878 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 819
 QY 619 ACGGCTCTTCATGAGCGGCGACGAGCGGCGGAGAGAGAGATGCCCTGTCTCAGA 678
 DB 818 ACGGCTCTTCATGAGCGGCGACGAGCGGCGGAGAGAGAGATGCCCTGTCTCAGA 759
 QY 679 AGGATGCTGTGAGCGCTCTGAGAGACAGTGTAGAGCAACGATATCCAGAGCCGAGT 738
 DB 758 AGGATGCTGTGAGCGCTCTGAGAGACAGTGTAGAGCAACGATATCCAGAGCCGAGT 700
 QY 739 CTAGCGCGCGCTCGGCGCGACCGAGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGGAGCG 798
 DB 699 CTAGCGCGCGCTCGGCGCGACCGAGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGGAGCG 640
 QY 799 CTTCACACGCTTCAGCGCCACCTATCTGATCTGACAGCAGATGACCTGCGCACCCAC 858
 DB 639 CTTCACACGCTTCAGCGCCACCTATCTGATCTGACAGCAGATGACCTGCGCACCCAC 580
 QY 859 CATCTGCTGTCAAGCGGAGAGAGCCCGACCTTACAGAGGCGCTGACCTCCAGCT 918
 DB 579 CTTCGCTGTCAAGCGGAGAGAGCCCGACCTTACAGAGGCGCTGACCTCCAGCT 520
 QY 919 TCGGAGACCGCGAGAGAGCTGGAACCTGAACCGGAGAGTGGGTGCGGCGACCCCAACAG 978
 DB 519 TCGGAGACCGCGAGAGAGCTGGAACCTGAACCGGAGAGTGGGTGCGGCGACCCCAACAG 460
 QY 979 AACCATCTTCAGACAGTACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1038
 DB 459 AACCATCTTCAGACAGTACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 400
 QY 1039 CAGTACTCGGCGCATGACGCGCACGTGCTACGCGAGCGGCGCATGGAGGGGCGCGCC 1098
 DB 399 CAGTACTCGGCGCATGACGCGCACGTGCTACGCGAGCGGCGCATGGAGGGGCGCGCC 340
 QY 1099 GCCACCTACAGAGGAGTCAATCGGCGCACTACCGGCGGCTCTCTTCAGACACGAGAG 1158
 DB 339 GCCACCTACAGAGGAGTCAATCGGCGCACTACCGGCGGCTCTCTTCAGACACGAGAG 280
 QY 1159 CAGTGGCGCGCGCTCTTGTGTGAGAGGAGCCCGGCTCC 1196
 DB 279 CAGTGGCGCGCGCTCTTGTGTGAGAGGAGCCCGGCTCC 242

RESULT 28 844 bp mRNA linear EST 15-JUL-2002
 B0686793
 LOCUS AGNCOURT_8345390 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6248044
 DEFINITION 5', mRNA sequence.
 ACCESSION B0686793
 VERSION B0686793.1 GI:21812109
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Euarhontoglires; Primates; Catarrhini;
 Homindaes; Homo.
 REFERENCE 1 (bases 1 to 844)
 AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LCM2387 row: e column: 05
High quality sequence stop: 593.
Location/Qualifiers

FEATURES

source

1. 844
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6248044"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site: 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

ORIGIN

Query Match 31.9%; Score 422; DB 5; Length 844;
Best Local Similarity 100.0%; Pred. No. 1.7e-196;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

900 GCCCTGCACTCCCTGCACTTGGGAGACCCGAGACAGAGTGAACCGGGAGTGG 959
1 GCCCTGCACTCCCTGCACTTGGGAGACCCGAGACAGAGTGAACCGGGAGTGG 60
960 TGGCGGACCCGCAACAGAACATCTTGACAGTGAAGTGAAGTGCACAGCTGG 1019
61 TGGCGGACCCGCAACAGAACATCTTGACAGTGAAGTGAAGTGCACAGCTGG 120
1020 GGGGCCCTGCCCCCGGAGAGTAACTCGGAGTCAAGCGCACTGCTACGGCAGCGG 1079
121 GGGGCCCTGCCCCCGGAGAGTAACTCGGAGTCAAGCGCACTGCTACGGCAGCGG 180
900 GGGCGATGAGGGGGCGCGCCGACCTTACAGAGAGTCACTGGCCACTACCGGGGTCT 1139
181 GGGCGATGAGGGGGCGCGCCGACCTTACAGAGAGTCACTGGCCACTACCGGGGTCT 240
1140 CTTTCAGACACGAGAGAGAGTGGGCGGCTCTTGCTGAGAGGGGACCGGGCTCAC 1199
241 CTTTCAGACACGAGAGAGAGTGGGCGGCTCTTGCTGAGAGGGGACCGGGCTCAC 300
900 ACAACACATCGCGCCCTTAGAGAGCGAGCATCTGAGCAAAAGAGATTAACAGA 1259
301 ACAACACATCGCGCCCTTAGAGAGCGAGCATCTGAGCAAAAGAGATTAACAGA 360
900 AAGAGACACCTCTTAGAGGTCCCGAGGGGGCGGGGTGGGGTGGTGAAGAAAGGC 1319
361 AAGAGACACCTCTTAGAGGTCCCGAGGGGGCGGGGTGGGGTGGTGAAGAAAGGC 420
900 1320 AG 1321
DB 421 AG 422

RESULT 29
BU157842 938 bp mRNA linear EST 04-SEP-2002
LOCUS BU157842
DEFINITION AGENCOURT_7976988 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6081573

5', mRNA sequence.
ACCESSION BU157842
VERSION BU157842.1 GI:22671752
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 938)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LCM2308 row: 1 column: 22
High quality sequence stop: 423.
Location/Qualifiers

FEATURES

source

1. 938
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6081573"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_110"
/note="Organ: pancreas; Vector: pOTB7; Site: 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

ORIGIN

Query Match 31.9%; Score 422; DB 5; Length 938;
Best Local Similarity 100.0%; Pred. No. 1.7e-196;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

900 GCCCTGCACTCCCTGCACTTGGGAGACCCGAGACAGAGTGAACCGGGAGTGG 959
1 GCCCTGCACTCCCTGCACTTGGGAGACCCGAGACAGAGTGAACCGGGAGTGG 60
960 TGGCGGACCCGCAACAGAACATCTTGACAGTGAAGTGAAGTGCACAGCTGG 1019
61 TGGCGGACCCGCAACAGAACATCTTGACAGTGAAGTGAAGTGCACAGCTGG 120
1020 GGGGCCCTGCCCCCGGAGAGTAACTCGGAGTCAAGCGCACTGCTACGGCAGCGG 1079
121 GGGGCCCTGCCCCCGGAGAGTAACTCGGAGTCAAGCGCACTGCTACGGCAGCGG 180
900 GGGCGATGAGGGGGCGCGCCGACCTTACAGAGAGTCACTGGCCACTACCGGGGTCT 1139
181 GGGCGATGAGGGGGCGCGCCGACCTTACAGAGAGTCACTGGCCACTACCGGGGTCT 240
1140 CTTTCAGACACGAGAGAGTGGGCGGCTCTTGCTGAGAGGGGACCGGGCTCAC 1199
241 CTTTCAGACACGAGAGAGTGGGCGGCTCTTGCTGAGAGGGGACCGGGCTCAC 300
900 ACAACACATCGCGCCCTTAGAGAGCGAGCATCTGAGCAAAAGAGATTAACAGA 1259
301 ACAACACATCGCGCCCTTAGAGAGCGAGCATCTGAGCAAAAGAGATTAACAGA 360
900 AAGAGACACCTCTTAGAGGTCCCGAGGGGGCGGGGTGGGGTGGTGAAGAAAGGC 1319
1260 AAGAGACACCTCTTAGAGGTCCCGAGGGGGCGGGGTGGGGTGGTGAAGAAAGGC 1319

Db 361 AAGGACACCTCTGTAGGGGTCCCAAGGGGGCCGGGCTGGGGCTGGAGTGAAGAGGC 420
Qy 1320 AG 1321
Db 421 AG 422

RESULT 30
BUI57959 952 bp mRNA linear EST 04-SEP-2002
LOCUS AGENCOURT_8076058 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6084984
DEFINITION BUI57959 5', mRNA sequence.
ACCESSION BUI57959
VERSION BUI57959.1 GI:22671869
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo
1 (bases 1 to 952)
NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgsabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM2317 row: k column: 01
High quality sequence stop: 607.
Location/Qualifiers
1..952
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6084984"
/issue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_110"
/note="Organ: pancreas; Vector: pOTB7; Site:1: XhoI;
Site:2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Query Match 31.9%; Score 422; DB 5; Length 952;
Best Local Similarity 100.0%; Pred. No. 1.7e-196;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 900 GCCCTGACACCTCTGTAGGGGTCCCAAGGGGGCCGGGCTGGAGTGAAGAGGC 959
Db 1 GCCCTGACACCTCTGTAGGGGTCCCAAGGGGGCCGGGCTGGAGTGAAGAGGC 60
Qy 960 TGGCGGCACCCCAAGAACATCTTGCAGAGTGAAGTGAATGATGTCAGAGGCTGG 1019
Db 61 TGGCGGCACCCCAAGAACATCTTGCAGAGTGAAGTGAATGATGTCAGAGGCTGG 120
Qy 1020 GGGGGCCCGCCCGCCGACAGTAACTGGGGCATGAGGCCACGCTTAAGGCGAGCGGCG 1079
Db 121 GGGGGCCCGCCCGCCGACAGTAACTGGGGCATGAGGCCACGCTTAAGGCGAGCGGCG 180
Qy 1080 GGGCGATGAGGGGGCGCGGCCCACTTAAGGAGGTGATGGCCACTTAAGCGGGGTCT 1139
Db 181 GGGCGATGAGGGGGCGCGGCCCACTTAAGGAGGTGATGGCCACTTAAGCGGGGTCT 240

Qy 1140 CTTTCAGACACGACAGAGAGTGGGGCCGCTCTTGTGCTGAGGGGACCCGGCTCCACC 1199
Db 241 CTTTCAGACACGACAGAGAGTGGGGCCGCTCTTGTGCTGAGGGGACCCGGCTCCACC 300
Qy 1200 ACACACATCGCGCCCTTGAAGAGCGCAGCCATCTGAGCAAAAGAGATTAACAGA 1259
Db 301 ACACACATCGCGCCCTTGAAGAGCGCAGCCATCTGAGCAAAAGAGATTAACAGA 360
Qy 1260 AAGGACACCTCTGTAGGGGTCCCAAGGGGGCCGGGCTGGGGCTGGAGTGAAGAGGC 1319
Db 361 AAGGACACCTCTGTAGGGGTCCCAAGGGGGCCGGGCTGGGGCTGGAGTGAAGAGGC 420

Qy 1320 AG 1321
Db 421 AG 422

RESULT 31
B0691500 1280 bp mRNA linear EST 15-JUL-2002
LOCUS AGENCOURT_9345477 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6248217
DEFINITION B0691500 5', mRNA sequence.
ACCESSION B0691500
VERSION B0691500.1 GI:21816816
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 1280)
NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgsabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM2387 row: 1 column: 10
High quality sequence stop: 423.
Location/Qualifiers
1..1280
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6248217"
/issue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_110"
/note="Organ: pancreas; Vector: pOTB7; Site:1: XhoI;
Site:2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Query Match 31.9%; Score 422; DB 5; Length 1280;
Best Local Similarity 100.0%; Pred. No. 1.6e-196;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 854 CCACCATCTTGGCTGTGAGAGGGGAGAGAGCCCACTTAAGAGGGGCCCTTGACCTTC 913
Db 28 CCACCATCTTGGCTGTGAGAGGGGAGAGAGCCCACTTAAGAGGGGCCCTTGACCTTC 87


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Seq primer: M13 FORWARD
POLYA=Yes.
location/Qualifiers
    source          1..629
FEATURES

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Db 421 TTCAGAGCATGAGATCAAGAGCTGAGATTGTTTC 457

RESULT 35
BM677602/c 730 bp mRNA linear EST 27-FEB-2002

LOCUS UI-E-EO1-aid-p-09-0-UI.s1 UI-E-EO1 Homo sapiens cDNA clone

DEFINITION UI-E-EO1-aid-p-09-0-UI 3', mRNA sequence.

ACCESSION BM677602

VERSION BM677602.1 GI:18987498

KEYWORDS EST. sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 730)

AUTHORS Ronaldo,M.F., Lennon,G. and Soares,M.B.

JOURNAL Normalization and subtraction: two approaches to facilitate gene

COMMENT 8889548

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@iowa.edu

Tissue Procurement: Dr. Gregg Hageman

cDNA library preparation: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com).

Seq primer: M13 Forward

POLYA=Yes.

Location/Qualifiers

1..730

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-E-EO1-aid-p-09-0-UI"

/tissue_type="fetal eye"

/dev_stage="fetal"

/lab_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone_lib="UI-E-EO1"

/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-EO1 is a normalized cDNA library containing the following tissue(s): fetal eye. The library was constructed according to Ronaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCGCTATACC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).

TAG TISSE=human fetal eye

TAG_LIB=UI-E-EO1

TAG_SEQ=CCGCTATACC"

ORIGIN

Query Match 30.4%; Score 401; DB 3; Length 730;
Best Local Similarity 99.5%; Pred. No. 3,9e-186;
Matches 551; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 768 TGCGGTGCGCCCTTTCAGGAGGAGGCTTCCACCGCTTCCAGCCCACTATCGT 827
DB 714 TGCGGTGCGCCCTTTCAGGAGGAGGCTTCCACCGCTTCCAGCCCACTATCGT 655
QY 828 ACTGACAGACAGAGATGACCTGACCCACCATCTGCTGTGACAGGGAGAGAGCCC 887
DB 654 ACTGACAGACAGAGATGACCTGACCCACCATCTGCTGTGACAGGGAGAGAGCCC 595
QY 888 CACCTTACAGAGGCGCTTGCACCTTCCAGCTTGGGAGAGAGAGAGAGAGAGAG 947
DB 594 CACCTTACAGAGGCGCTTGCACCTTCCAGCTTGGGAGAGAGAGAGAGAGAGAG 535
QY 948 ACCGGAGTGGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1007
DB 534 ACCGGAGTGGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 475
QY 1008 GTGCGAGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1067
DB 474 GTGCGAGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 415
QY 1068 AGGCGAGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1127
DB 414 AGGCGAGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 355
QY 1128 ACCGGAGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1187
DB 354 ACCGGAGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 295
QY 1188 CCGGCTTCAC 1247
DB 294 CCGGCTTCAC 235
QY 1248 AGATTAACAGAAAGAGACACCTCTCTAGAGGTCCCAAGAGAGAGAGAGAG 1307
DB 234 AGATTAACAGAAAGAGACACCTCTCTAGAGGTCCCAAGAGAGAGAGAGAG 175
QY 1308 AGGTGAAGAGGAG 1321
DB 174 AGGTGAAGAGGAG 161

RESULT 36
LOCUS BM974296/c 626 bp mRNA linear EST 20-FEB-2003
DEFINITION UI-CF-EC1-aca-k-23-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
ACCESSION BM974296
VERSION BM974296.1 GI:19591887
KEYWORDS EST. sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 626)
AUTHORS Ronaldo,M.F., Lennon,G. and Soares,M.B.
TITLES Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
PUBMED 8889548
COMMENT Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@iowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA library preparation: Dr. M. Bento Soares, University of Iowa
cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems

ACCESSION BU683523
 VERSION BU683523.1 GI:23535533
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 728)
 AUTHORS Ronaldo, M.F., Lennon, G. and Soares, M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 PUBMED 8889548
 COMMENT Contact: McCray, PB
 McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).
 Seq primer: M13 FORWARD
 POLYA=yes.
 FEATURES
 source
 1..728
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-CF-ECL-acg-e-09-0-UI"
 /tissue_type="lung"
 /dev_stage="Adult and Fetal"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-CF-ECL"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-CF-ECL is a normalized cDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Ronaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AAGTGGCTTAC.
 TAG TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371 and 380-383
 TAG LIB=UI-CF-ECL
 TAG_SEQ=AAGTGGCTTAC"

ORIGIN

Query Match 29.8%; Score 393; DB 5; Length 728;
 Best Local Similarity 99.8%; Pred. No. 3.4e-182;
 Matches 443; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 878 GAGAGACCCCTACCTACCGAGGCCCCCTTGCAGCTTCAGTTGGAGACCCCGAGCAGCAG 937
 DB 603 GAGAGACCCCTACCTACCGAGGCCCCCTTGCAGCTTCAGTTGGAGACCCCGAGCAGCAG 544
 QY 938 CTGGAACCTGAACCGGAGAGTCGGTGGCGGACCCCGAAAGACCATCTTCGACAGTGCAC 997
 DB 543 CTGGAACCTGAACCGGAGAGTCGGTGGCGGACCCCGAAAGACCATCTTCGACAGTGCAC 484

QY 998 CTGATGATATGTGCACAGCTGGGCGGCCCTGCGCCCGCCAGACATACTCGGAGTACGC 1057
 DB 483 CTGATGATATGTGCACAGCTGGGCGGCCCTGCGCCCGCCAGACATACTCGGAGTACGC 424
 QY 1058 GCCACGTGTACACGACCGGCGGCGCATGAGAGGCGCGCCGCCACTTACAGCGAGGTC 1117
 DB 423 GCCACGTGTACACGACCGGCGGCGCATGAGAGGCGCGCCGCCACTTACAGCGAGGTC 364
 QY 1118 ATCGGCACTACCGCGGGTCTCTCTTCCAGACACAGAGACAGTGGCGGCGCCCTCTTG 1177
 DB 363 ATCGGCACTACCGCGGGTCTCTCTTCCAGACACAGAGACAGTGGCGGCGCCCTCTTG 304
 QY 1178 CTGAGAGGGGACCGGCTCCACACACACATCGCGCCCTAGAGAGCGCAGCATCTGG 1237
 DB 303 CTGAGAGGGGACCGGCTCCACACACACATCGCGCCCTAGAGAGCGCAGCATCTGG 244
 QY 1238 AGCAAGAGAGAGATTAACAGAAAGACACCTCTTAGAGTCCCAAGGCGGCGCGGCT 1297
 DB 243 AGCAAGAGAGAGATTAACAGAAAGACACCTCTTAGAGTCCCAAGGCGGCGCGGCT 184
 QY 1298 GGGGCTGGCTAGTGAAGAGCAG 1321
 DB 183 GGGGCTGGCTAGTGAAGAGCAG 160

RESULT 39

BU169156 973 bp mRNA linear EST 04-SEP-2002
 AGENCOURT 7975486 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6082799
 LOCUS
 DEFINITION 5', mRNA sequence.

ACCESSION BU169156
 VERSION BU169156.1 GI:22683140
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 973)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgsabbs-remail.nih.gov
 Tissue Procurement: ATCC

cDNA library Preparation: Rubin Laboratory
 cDNA library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at:
 http://image.llnl.gov
 Plate: ILN2311 row: 0 column: 24
 High quality sequence stop: 500.

FEATURES

source

1..973
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6082799"
 /tissue_type="ductal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_110"
 /note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

AUTHORS NCI-CCAP <http://www.ncbi.nlm.nih.gov/nciccap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-rt@mail.nih.gov
 CDNA Library Preparation:
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC)
 Clone distribution: NCI-CCAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
info@image.llnl.gov
 Plate: L14M8009 row: E column: 1
 Seq primer: M13R1 reverse primer (ABI).
 Location/Qualifiers

FEATURES
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3271656"
 /sex="male"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
 with a modified polylinker; Plasmid DNA from the
 normalized library NCI CGAP Pr22 was prepared, and as
 circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clonoids
 985608-986759, 1101192-1101959, and 1217928-1220615).
 Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 28.5%; Score 377; DB 6; Length 563;
 Best Local Similarity 100.0%; Pred. No. 2.7e-174;
 Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

945 TGAACCGGAGTGGTGGCGGCGACCCCAAGAACATCTTCGACAGTGAAGTATG 1004
 10 TGAACCGGAGTGGTGGCGGCGACCCCAAGAACATCTTCGACAGTGAAGTATG 69
 QY 1005 ATAGTCCAGGCTGGGCGGCGCCCTGCGCCAGAGTAATCTCGGCACTACGCGCAGT 1064
 DB 70 ATAGTCCAGGCTGGGCGGCGCCCTGCGCCAGAGTAATCTCGGCACTACGCGCAGT 129
 QY 1065 GCTACGGCGGCGGCGGCGCGATGAGGGCGCGCCCACTACAGCGAGTCACTGGCC 1124
 DB 130 GCTACGGCGGCGGCGGCGCGATGAGGGCGCGCCCACTACAGCGAGTCACTGGCC 189
 QY 1125 ACTACCGGCGGCTCTCTTCGACGACCGAGAGAGTGGGCGCGCTCTCTGCTGGAGG 1184
 DB 190 ACTACCGGCGGCTCTCTTCGACGACCGAGAGAGTGGGCGCGCTCTCTGCTGGAGG 249
 QY 1185 GGACCGGCTCCACACACACATCGCGCCCTTAGAGAGCGCAGCATCTGAGCAAG 1244
 DB 250 GGACCGGCTCCACACACACATCGCGCCCTTAGAGAGCGCAGCATCTGAGCAAG 309
 QY 1245 AGAAGGATTAACAGAAAGACACCTCTCTAGGGTCCCGAGGGCGGCGCTGGGGCTG 1304
 DB 310 AGAAGGATTAACAGAAAGACACCTCTCTAGGGTCCCGAGGGCGGCGCTGGGGCTG 369
 QY 1305 CGTAGGTGAAAAGCGAG 1321
 DB 370 CGTAGGTGAAAAGCGAG 386

RESULT 42
 LOCUS BM13900 552 bp mRNA linear EST 28-FEB-2002
 DEFINITION UI-E-EJ0-abq-e-07-0-UI.r1 UI-E-EJ0 Homo sapiens CDNA clone.

ACCESSION UI-E-EJ0-abq-e-07-0-UI.5', mRNA sequence.
VERSION BM13900
KEYWORDS EST.
SOURCE GI:19027158
ORGANISM Homo sapiens (human)

REFERENCE Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo
 1 (bases 1 to 552)
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)

JOURNAL 889348
PUBMED
COMMENT Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9365
 Email: bento-soares@uiowa.edu
 Tissue Procurement: Dr. Gregg Hageman
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).
 The following repetitive elements were found in this CDNA
 sequence: 521-543, >POLY_A#Simple_repeat
 Seq primer: M13 Reverse.

FEATURES

source

1..552
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-E-EJ0-abq-e-07-0-UI"
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 optic nerve, retina, Retina Foveal and Macular, RPE and
 Choroid"
 /dev_stage="fetal and adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-E-EJ0"
 /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
 modified polylinker; Site_1: EcoR I; Site_2: Not I;
 UI-E-EJ0 is a subtracted CDNA library constructed
 according to Bonaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand CDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an EcoR I adaptor, digested
 with Not I, and cloned directionally into pT7T3-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand CDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tags for this library are: fetal eyes,
 AGATTCAGAG, lens, CGATTAGCGA, eye anterior segment,
 AATCCCGCAT, optic nerve, CCATTAGTGT, retina, CCGCG,
 Foveal and Macular, GTCC, RPE and Choroid, ACTGA. This
 library was created for the program, Gene Discovery in the
 Visual System, supported by National Eye Institute (NEI)."

ORIGIN

Query Match 27.6%; Score 365; DB 3; Length 552;
 Best Local Similarity 100.0%; Pred. No. 2.3e-168;
 Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

944 CTGAACCGGAGTGGTGGCGGCGACCCCAAGAACATCTTCGACAGTGAAGTATG 1003
 1 CTGAACCGGAGTGGTGGCGGCGACCCCAAGAACATCTTCGACAGTGAAGTATG 60
 QY 1004 GATAGTGCAGGCTGGGCGGCGCCCTGCGCCAGAGTAATCTCGGCGATCAGGCGCAG 1063
 DB 61 GATAGTGCAGGCTGGGCGGCGCCCTGCGCCAGAGTAATCTCGGCGATCAGGCGCAG 120

QY 1064 TGCTACGGCAGCCGGGCGGCGATGAGAGGGGCGCCGCCCACTTACAGAGAGTCATGGC 1123
 DB 121 TGCTACGGCAGCCGGGCGGCGCATGAGAGGGGCGCGCCCACTTACAGAGAGTCATGGC 180
 QY 1124 CACTACCGGGGGTCTCTCTTCCAGACACGAGAGAGTGGGCGCCCTCTTCTCTGAG 1183
 DB 181 CACTACCGGGGGTCTCTCTTCCAGACACGAGAGAGTGGGCGCCCTCTTCTCTGAG 240
 QY 1184 GGAACCGGGCTTCCACACACATCGCGCCCTTGAAGAGCGAGCCATCTGAGCAAA 1243
 DB 241 GGAACCGGGCTTCCACACACATCGCGCCCTTGAAGAGCGAGCCATCTGAGCAAA 300
 QY 1244 GAGAAGATTAACAGAAAGACACCTCTTCTTGAAGTCCCGGAGGGGCGCGGCT 1303
 DB 301 GAGAAGATTAACAGAAAGACACCTCTTCTTGAAGTCCCGGAGGGGCGCGGCT 360
 QY 1304 GCGTA 1308
 DB 361 GCGTA 365

RESULT 43
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 DEFINITION AGENCOURT_8045602 NIH_MGC_110 Homo sapiens CDNA clone IMAGE:6085305
 5', mRNA sequence.
 ACCESSION BUI74654
 VERSION BUI74654.1 GI:22688638
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 1127)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: L1CM2318 row: h column: 10
 High quality sequence start: 159
 High quality sequence stop: 554.
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 /clone="IMAGE:6085305"
 /tissue_type="ductal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_1ib="NIH MGC 110"
 /note="Organ: pancreas; Vector: pORF7; Site_1: XhoI;
 Site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCAAGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 27.1%; Score 358; DB 5; Length 1127;
 Best Local Similarity 99.8%; Pred. No. 6,2e-165;
 Matches 408; Conservativg 0; Mismatches 1; Indels 0; Gaps 0;

QY 522 CGGAGCTGAGATTGTTTCAGATCATCATGCTGAGGAGATGATGATGATGATG 581
 DB 229 CGGAGCTGAGATTGTTTCAGATCATCATGCTGAGGAGATGATGATGATGATG 288
 QY 582 TGATCAAGTGTCTGTAGAGCACTAACAGTGTCTGACAGGTCTTTCATCAGCGGAC 641
 DB 289 TGATCAAGTGTCTGTAGAGCACTAACAGTGTCTGACAGGTCTTTCATCAGCGGAC 348
 QY 642 GCCAGGGGCGGAGAGAGAAAGATGCTTGTCTTCAAGAGATGCTGTGCTCGGAGA 701
 DB 349 GCCAGGGGCGGAGAGAGAAAGATGCTTGTCTTCAAGAGATGCTGTGCTCGGAGA 408
 QY 702 GCACAGTGTAGGCAACGGATTCGAGAGCGGAGGTTACAGCCCGGCTCGGACCG 761
 DB 409 GCACAGTGTAGGCAACGGATTCGAGAGCGGAGGTTACAGCCCGGCTCGGACCG 468
 QY 762 ACCGCTGCGCGTGTGCGCCCTTCCAGCGGAGCGCTTCCACCGCTTCCAGCCGACT 821
 DB 469 ACCGCTGCGCGTGTGCGCCCTTCCAGCGGAGCGCTTCCACCGCTTCCAGCCGACT 528
 QY 822 ATCGTACTGACAGACAGAGATGACCTGCGACCCACCATCTGCTGACAGCGGAGG 881
 DB 529 ATCGTACTGACAGACAGAGATGACCTGCGCGCCACCATCTGCTGACAGCGGAGG 588
 QY 882 AGCCCCAGCCCTACAGAGGCGCCCTGACAGCTTGGGAGACCCGGA 930
 DB 589 AGCCCCAGCCCTACAGAGGCGCCCTGACAGCTTGGGAGACCCGGA 637

RESULT 44
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 DEFINITION AGENCOURT_10442327 NIH_MGC_107 Homo sapiens CDNA clone
 IMAGE:6650815 5', mRNA sequence.
 ACCESSION BUI59841
 VERSION BUI59841.1 GI:24044833
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 646)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: L1CM2896 row: k column: 07
 High quality sequence stop: 551.
 Location/Qualifiers
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 /tissue_type="adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_1ib="NIH MGC 107"
 /note="Organ: breast; Vector: pORF7; Site_1: EcoRI;
 Site_2: XhoI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCAAGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit

FEATURES
 source

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2006, 10:09:56 ; Search time 275 Seconds
(without alignments)
8538,760 Million cell updates/sec

Title: US-09-934-249-1

Perfect score: 1321
Sequence: 1 cgaccgcgcttcgagcga.....ctcgcgtagctgaagacag 1321

Scoring table: OLIGO NUC
Gapop 60.0, Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size: 23

Total number of hits satisfying chosen parameters: 354

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

Database:

Issued Patents NA:*

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- 2: /cgn2_6/prodata/1/ina/5_COMB.seq:*
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- 5: /cgn2_6/prodata/1/ina/H_COMB.seq:*
- 6: /cgn2_6/prodata/1/ina/PP_COMB.seq:*
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- 9: /cgn2_6/prodata/1/ina/backfillseq.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	800	60.6	US-09-769-482-1	Sequence 1, Appl1
2	755	57.2	US-09-769-482-2	Sequence 2, Appl1
3	34	2.6	US-09-640-211A-146	Sequence 146, App
4	31	2.3	US-09-640-211A-1198	Sequence 1198, Ap
5	31	2.3	US-09-640-211A-1340	Sequence 1340, Ap
6	31	2.3	US-10-104-047-700	Sequence 700, App
7	30	2.3	US-09-949-016-13247	Sequence 13247, A
8	30	2.3	US-09-949-016-15127	Sequence 15127, A
9	29	2.2	US-09-949-016-1263	Sequence 1263, Ap
10	29	2.2	US-09-949-016-13005	Sequence 13005, A
11	29	2.2	US-09-949-016-17419	Sequence 17419, A
12	29	2.2	US-09-949-016-12052	Sequence 12052, A
13	29	2.2	US-09-949-016-1765	Sequence 1765, A
14	28	2.1	US-09-886-010-1	Sequence 1, Appl1
15	28	2.1	US-09-886-010-1	Sequence 1, Appl1
16	28	2.1	US-09-879-312A-1	Sequence 1, Appl1
17	28	2.1	US-07-705-490-1	Sequence 1, Appl1
18	28	2.1	US-07-751-891B-1	Sequence 1, Appl1
19	28	2.1	US-08-455-073A-1	Sequence 1, Appl1
20	28	2.1	US-08-457-273B-41	Sequence 41, Appl1
21	28	2.1	US-08-556-419-13	Sequence 13, Appl1
22	28	2.1	US-09-041-886-14	Sequence 14, Appl1
23	28	2.1	US-08-246-982A-5	Sequence 5, Appl1
24	28	2.1	US-08-453-265-5	Sequence 5, Appl1

25	2.1	43117	3	US-09-949-016-17589	Sequence 17589, A
26	2.0	402	3	US-09-854-133-418	Sequence 418, App
27	2.0	8983	3	US-09-949-016-15437	Sequence 15437, A
28	2.0	154746	3	US-09-827-668-8	Sequence 8, Appl1
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30	2.0	367	3	US-09-325-932A-2	Sequence 2, Appl1
31	2.0	601	3	US-09-949-016-16860	Sequence 46860, A
32	2.0	641	3	US-09-436-699C-5	Sequence 5, Appl1
33	2.0	1719	3	US-09-436-699C-19	Sequence 19, Appl1
34	2.0	1740	3	US-09-922-364A-15	Sequence 15, Appl1
35	2.0	1740	3	US-09-922-364A-15	Sequence 15, Appl1
36	2.0	1740	3	US-09-254-550-15	Sequence 15, Appl1
37	2.0	1740	3	US-10-115-415-15	Sequence 15, Appl1
38	2.0	1740	3	US-10-115-671-15	Sequence 15, Appl1
39	2.0	1740	3	US-10-115-695-15	Sequence 15, Appl1
40	2.0	1877	3	US-09-780-133A-10	Sequence 10, Appl1
41	2.0	2832	3	US-08-819-177-2	Sequence 2, Appl1
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44	2.0	2953	3	US-09-402-214-1	Sequence 1, Appl1
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47	2.0	3725	3	US-09-799-451-260	Sequence 260, App
48	2.0	4412	3	US-09-949-016-1656	Sequence 5656, Ap
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51	2.0	9308	3	US-09-949-016-13107	Sequence 13107, A
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53	2.0	29960	3	US-09-949-016-16100	Sequence 16100, A
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55	2.0	31842	3	US-09-949-016-15123	Sequence 15123, A
56	2.0	33675	3	US-09-921-992-2	Sequence 2, Appl1
57	2.0	139150	3	US-09-949-016-17398	Sequence 17398, A
58	2.0	139577	3	US-09-949-016-12879	Sequence 12879, A
59	2.0	196942	3	US-09-949-016-13209	Sequence 13209, A
60	2.0	254405	3	US-09-949-016-14381	Sequence 14381, A
61	1.9	152	3	US-09-513-999C-8786	Sequence 8786, Ap
62	1.9	451	3	US-09-357-755-3	Sequence 3, Appl1
63	1.9	457	2	US-08-332-766A-7	Sequence 7, Appl1
64	1.9	720	3	US-09-664-958-2	Sequence 2, Appl1
65	1.9	1083	2	US-08-319-866-1	Sequence 1, Appl1
66	1.9	1083	3	US-08-809-917-1	Sequence 1, Appl1
67	1.9	1083	3	US-09-419-371-1	Sequence 1, Appl1
68	1.9	1764	3	US-09-664-958-13	Sequence 13, Appl1
69	1.9	2961	3	US-10-104-047-488	Sequence 488, App
70	1.9	4415	3	US-09-949-002-24	Sequence 24, Appl1
71	1.9	22118	3	US-09-815-981A-5	Sequence 5, Appl1
72	1.9	35630	3	US-09-949-016-13832	Sequence 13832, A
73	1.9	75929	3	US-09-949-016-15544	Sequence 15544, A
74	1.9	106315	3	US-09-949-016-16613	Sequence 16613, A
75	1.9	106315	3	US-09-949-016-16613	Sequence 16613, A
76	1.9	137000	3	US-10-172-911-11	Sequence 11, Appl1
77	1.8	30	3	US-09-475-981A-332	Sequence 332, Appl1
78	1.8	416	3	US-09-370-838-249	Sequence 249, App
79	1.8	416	3	US-09-854-133-359	Sequence 359, App
80	1.8	431	3	US-09-854-133-359	Sequence 359, App
81	1.8	511	3	US-10-178-213-373	Sequence 373, App
82	1.8	520	3	US-09-228-986-42	Sequence 42, Appl1
83	1.8	595	3	US-10-101-464A-42	Sequence 42, Appl1
84	1.8	595	3	US-10-101-464A-42	Sequence 1, Appl1
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86	1.8	1809	3	US-08-393-465-1	Sequence 1, Appl1
87	1.8	1809	3	PCT-US95-11869-1	Sequence 1, Appl1
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89	1.8	2956	3	US-09-999-833A-89	Sequence 89, Appl1
90	1.8	2956	3	US-10-020-445A-89	Sequence 89, Appl1
91	1.8	3313	3	US-09-964-899-52	Sequence 52, Appl1
92	1.8	18079	3	US-09-949-016-13344	Sequence 13344, A
93	1.8	70383	3	US-10-283-247-3	Sequence 3, Appl1
94	1.8	119762	3	US-09-949-016-17313	Sequence 17313, A
95	1.7	25	2	US-08-374-144-3	Sequence 3, Appl1
96	1.7	25	2	US-08-374-144-3	Sequence 3, Appl1
97	1.7	25	2	US-08-775-164-3	Sequence 3, Appl1

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99	23	1.7	25	2	US-08-775-607-3	Sequence 3, Appli	172	23	1.7	1393	3	US-09-626-896-24	Sequence 24, Appl
100	23	1.7	25	6	PCT-US93-06828-3	Sequence 3, Appli	173	23	1.7	1393	3	US-09-485-046-15	Sequence 15, Appl
101	23	1.7	27	3	US-09-590-211A-3	Sequence 3, Appli	174	23	1.7	1393	3	US-09-841-730-24	Sequence 24, Appl
102	23	1.7	30	2	US-08-068-747-2	Sequence 2, Appli	175	23	1.7	1437	3	US-10-200-012-7	Sequence 7, Appli
103	23	1.7	30	3	US-09-590-211A-4	Sequence 4, Appli	176	23	1.7	1500	3	US-09-902-540-7578	Sequence 7578, Ap
104	23	1.7	33	2	US-08-068-747-7	Sequence 7, Appli	177	23	1.7	1617	3	US-09-444-336-4	Sequence 4, Appli
105	23	1.7	33	3	US-09-590-211A-5	Sequence 5, Appli	178	23	1.7	1617	3	US-10-093-045-4	Sequence 4, Appli
106	23	1.7	33	3	US-09-590-211A-6	Sequence 6, Appli	179	23	1.7	1617	3	US-10-093-246-4	Sequence 4, Appli
107	23	1.7	36	3	US-09-590-211A-7	Sequence 7, Appli	180	23	1.7	1617	3	US-10-018-902-25	Sequence 25, Appl
108	23	1.7	39	3	US-09-590-211A-8	Sequence 8, Appli	181	23	1.7	1643	3	US-09-799-451-667	Sequence 667, App
109	23	1.7	42	3	US-09-590-211A-9	Sequence 9, Appli	182	23	1.7	1659	3	US-09-083-351-3	Sequence 3, Appli
110	23	1.7	45	3	US-09-497-933A-22	Sequence 22, Appli	183	23	1.7	1659	3	US-09-083-352-3	Sequence 3, Appli
111	23	1.7	45	3	US-09-590-211A-9	Sequence 9, Appli	184	23	1.7	1660	3	US-09-949-016-1424	Sequence 1424, Ap
112	23	1.7	48	3	US-09-497-933A-19	Sequence 19, Appli	185	23	1.7	1662	3	US-09-612-809B-3	Sequence 3, Appli
113	23	1.7	60	3	US-09-497-933A-21	Sequence 21, Appli	186	23	1.7	1759	2	US-08-765-868A-1	Sequence 1, Appli
114	23	1.7	63	3	US-09-497-933A-18	Sequence 18, Appli	187	23	1.7	1917	3	US-09-799-451-520	Sequence 520, App
115	23	1.7	63	3	US-09-497-933A-23	Sequence 23, Appli	188	23	1.7	1992	3	US-09-799-451-521	Sequence 521, App
116	23	1.7	63	3	US-09-497-933A-25	Sequence 25, Appli	189	23	1.7	2227	3	US-09-949-016-3895	Sequence 3895, Ap
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118	23	1.7	69	3	US-08-480-173A-32	Sequence 32, Appli	191	23	1.7	2308	3	US-09-395-115-9	Sequence 9, Appli
119	23	1.7	69	3	US-08-484-408A-31	Sequence 31, Appli	192	23	1.7	2308	3	US-08-436-265-9	Sequence 9, Appli
120	23	1.7	69	3	US-08-484-408A-32	Sequence 32, Appli	193	23	1.7	2308	3	US-09-679-187-9	Sequence 9, Appli
121	23	1.7	78	3	US-09-573-080A-464	Sequence 464, App	194	23	1.7	2308	3	US-09-267-963D-9	Sequence 9, Appli
122	23	1.7	81	3	US-09-497-933A-24	Sequence 24, Appli	195	23	1.7	2308	3	US-09-949-016-657	Sequence 657, App
123	23	1.7	90	3	US-09-497-933A-20	Sequence 20, Appli	196	23	1.7	2400	3	US-10-104-047-228	Sequence 228, App
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150	23	1.7	726	3	US-09-854-133-462	Sequence 462, App	223	23	1.7	3715	3	US-09-557-262-11	Sequence 11, Appl
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RESULT 1

US-09-769-482-1

Sequence 1, Application US/09769482

Patent No. 6566130

GENERAL INFORMATION:

APPLICANT: SRIVASTAVA, SHIV

APPLICANT: MOULI, JUDD W.

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TITLE OF INVENTION: POUYUCLEOTIDE ARRAY

TITLE OF INVENTION: POUYUCLEOTIDE ARRAY

FILE REFERENCE: 04995, 0057-00000

CURRENT APPLICATION NUMBER: US/09/769,482

CURRENT FILING DATE: 2001-01-26

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PRIOR APPLICATION NUMBER: 60/179,045

PRIOR FILING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 67

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 1140

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (95)..(850)

US-09-769-482-1

ALIGNMENTS

60.6%; Score 800; DB 3; Length 1140;

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Patent No. 6833446
GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 146
LENGTH: 640
TYPE: DNA
ORGANISM: Eucalyptus grandis
US-09-640-211A-146

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RESULT 4
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Sequence 1198, Application US/09640211A
Patent No. 6833446
GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
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Patent No. 6833446
GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
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NUMBER OF SEQ ID NOS: 2368
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US-09-640-211A-1340

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Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-10-104-047-700/C
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Patent No. 6943241
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. 6943241e1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 700
LENGTH: 2332
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ORGANISM: Homo sapiens
US-10-104-047-700

Query Match
Best Local Similarity 100.0%; Pred. No. 0.00097;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1225 GAGGAGGAGGAGCGCGCGCGCGCGCGCGCG 1195

RESULT 7
US-09-949-016-13247
Sequence 13247, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13247
LENGTH: 11729
TYPE: DNA
ORGANISM: Human
US-09-949-016-13247

Query Match
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 30; DB 3; Length 11729;
```


Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 45 GAGGAGGAGAGCGCGCGCGCGCG 74
Db 10019 GAGGAGGAGAGCGCGCGCGCGCG 10048

RESULT 8
US-09-949-016-15127
Sequence 15127, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15127
LENGTH: 142783
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(142783)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15127

Query Match 2.3%; Score 30; DB 3; Length 142783;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 554 GTGGTGATGATGATGATGATGATG 583
Db 23669 GTGGTGATGATGATGATGATG 23658

RESULT 9
US-09-949-016-1263/C
Sequence 1263, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1263
LENGTH: 3430
TYPE: DNA
ORGANISM: Human
US-09-949-016-1263

Query Match 2.2%; Score 29; DB 3; Length 3430;
Best Local Similarity 100.0%; Pred. No. 0.0069;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 557 GTGGTATGATGATGATGATGATGAT 585
Db 802 GTGGTATGATGATGATGATGATGAT 774

RESULT 10
US-09-949-016-13005/C
Sequence 13005, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13005
LENGTH: 9406
TYPE: DNA
ORGANISM: Human
US-09-949-016-13005

Query Match 2.2%; Score 29; DB 3; Length 9406;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 557 GTGGTATGATGATGATGATGATGAT 585
Db 2802 GTGGTATGATGATGATGATGATGAT 2774

RESULT 11
US-09-949-016-17419/C
Sequence 17419, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17419
LENGTH: 13832
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(13832)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17419

Query Match 2.2%; Score 29; DB 3; Length 13832;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 TGAGAGAGAGAGCGCGCGCGCG 72
DB 1875 TGAGAGAGAGAGCGCGCGCGCG 1847

RESULT 12
US-09-949-016-12052/C
Sequence 12052, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12052
LENGTH: 34230
TYPE: DNA
ORGANISM: Human
US-09-949-016-12052

Query Match 2.2%; Score 29; DB 3; Length 34230;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 555 TGGTGTGATGATGATGATGATGATG 583
DB 4653 TGGTGTGATGATGATGATGATGATG 4625

RESULT 13
US-09-949-016-13765/C
Sequence 13765, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13765
LENGTH: 128470
TYPE: DNA
ORGANISM: Human
US-09-949-016-13765

Query Match 2.2%; Score 29; DB 3; Length 128470;
Best Local Similarity 100.0%; Pred. No. 0.005; Mismatches 0; Indels 0; Gaps 0;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 555 TGGTGTGATGATGATGATGATGATG 583
DB 98598 TGGTGTGATGATGATGATGATGATG 98570

RESULT 14
US-09-236-097-7
Sequence 7, Application US/09236097
Patent No. 635165
GENERAL INFORMATION:
APPLICANT: NIR NAVOT ET AL
TITLE OF INVENTION: METHODS AND KITS FOR CHARACTERIZING GC
TITLE OF INVENTION: -RICH NUCLEIC ACID SEQUENCES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 20001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted to
SOFTWARE: an ASCII file
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,097
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 128/33
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 700
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-236-097-7

Query Match 2.1%; Score 28; DB 3; Length 700;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 GCGCGCGCGCGCGCGCGCGCGCG 83
DB 505 GCGCGCGCGCGCGCGCGCGCGCG 532

RESULT 15
US-09-086-010-1
Sequence 1, Application US/09086010
Patent No. 6274338
GENERAL INFORMATION:
APPLICANT: Glimcher, Laurie H. et al.
TITLE OF INVENTION: Human C-Maf Compositions and
TITLE OF INVENTION: Methods of Use Thereof
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk


```
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/086,010
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/030,579
FILING DATE: 2-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Kara, Catherine J.
REGISTRATION NUMBER: 41,106
REFERENCE/DOCKET NUMBER: HUI-027CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1203 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1203
US-09-086-010-1
```

```
Query Match 2.1%; Score 28; DB 3; Length 1203;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 56 GCGCGCGCGCGCGCGCGCGCGCGAGCG 83
DB 679 GCGCGCGCGCGCGCGCGCGCGCGAGCG 706
```

```
RESULT 16
US-09-879-312A-1
Sequence 1, Application US/09879312A
Patent No. 6933125
GENERAL INFORMATION:
APPLICANT: DOUGAN III, JOHN
TITLE OF INVENTION: HUMAN C-MAF COMPOSITIONS AND METHODS OF USE THEREFOR
FILE REFERENCE: HUI-027CPV1
CURRENT APPLICATION NUMBER: US/09/879,312A
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: 09/086,010
PRIOR FILING DATE: 1998-05-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 1
LENGTH: 1203
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1203)
US-09-879-312A-1
```

```
Query Match 2.1%; Score 28; DB 3; Length 1203;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 56 GCGCGCGCGCGCGCGCGCGCGCGAGCG 83
DB 679 GCGCGCGCGCGCGCGCGCGCGCGAGCG 706
```

```
RESULT 17
US-07-705-490-1
```

```
Sequence 1, Application US/07705490
Patent No. 6107025
GENERAL INFORMATION:
APPLICANT: Caskey, C. T.
APPLICANT: Nelson, David L.
APPLICANT: Pieretti, Maura
APPLICANT: Warren, Stephen T.
TITLE OF INVENTION: Diagnosis of the Fragile X Syndrome
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thomas D. Paul
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/705,490
FILING DATE: 19910708
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5350
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
TELEX: 762829
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3765 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-705-490-1
```

```
Query Match 2.1%; Score 28; DB 3; Length 3765;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 56 GCGCGCGCGCGCGCGCGCGCGCGAGCG 83
DB 44 GCGCGCGCGCGCGCGCGCGCGCGAGCG 71
```

```
RESULT 18
US-07-751-891B-1
Sequence 1, Application US/07751891B
Patent No. 6180337
GENERAL INFORMATION:
APPLICANT: Caskey, C. T.
APPLICANT: Nelson, David L.
APPLICANT: Pieretti, Maura
APPLICANT: Warren, Stephen T.
TITLE OF INVENTION: Diagnosis of the Fragile X Syndrome
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thomas D. Paul
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
```


ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/751,891B
FILING DATE: 29-Aug-1991
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5350
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
TELEX: 762829
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3765 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-07-751-891B-1

Query Match 2.1%; Score 28; DB 3; Length 3765;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 GCGCGCGCGCGCGCGCGCGCGCGGAGCG 83
DB 44 GCGCGCGCGCGCGCGCGCGCGCGGAGCG 71

RESULT 19
US-08-455-073A-1
Sequence 1, Application US/08455073A
Patent No. 5876949
GENERAL INFORMATION:
APPLICANT: Gideon Dreyfus
APPLICANT: Mikiko C. Stomi
APPLICANT: Yan Zhang
TITLE OF INVENTION: Fragile X Related Proteins, Compositions And Methods
TITLE OF INVENTION: Of Making And Using The Same
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5876949ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,073A
FILING DATE: 31-May-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-2201
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4362 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 220..2118
US-08-455-073A-1

Query Match 2.1%; Score 28; DB 2; Length 4362;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 GCGCGCGCGCGCGCGCGCGCGCGGAGCG 83
DB 68 GCGCGCGCGCGCGCGCGCGCGCGGAGCG 95

RESULT 20
US-08-457-273B-41/c
Sequence 41, Application US/08457273B
Patent No. 5849995
GENERAL INFORMATION:
APPLICANT: Hayden, Michael
APPLICANT: Lin, Biaoyang
APPLICANT: Nasir, Jamal
TITLE OF INVENTION: Mouse Model for Huntington's Disease and
TITLE OF INVENTION: Related DNA Sequences
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSER: Virginia Bennett
STREET: PO Box 37428
CITY: Raleigh
STATE: No. 584995th Carolina
COUNTRY: US
ZIP: 27627
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,273B
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Virginia C.
REGISTRATION NUMBER: 37,092
REFERENCE/DOCKET NUMBER: 3477-85A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-854-1400
TELEFAX: 919-854-1401
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 10348 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-457-273B-41

Query Match 2.1%; Score 28; DB 2; Length 10348;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GAGGAGCGCGCGCGCGCGCGCGGCGG 78
DB 469 GAGGAGCGCGCGCGCGCGCGCGGCGG 442

RESULT 21
US-08-556-419-13/c
Sequence 13, Application US/08556419C
Patent No. 6093549
GENERAL INFORMATION:
APPLICANT: Ross, Christopher
APPLICANT: Li, Xiao-Jiang
APPLICANT: Li, Shi-Hua
APPLICANT: Sharp, Alan
APPLICANT: Lanahan, Anthony
APPLICANT: Worley, Paul
APPLICANT: Snyder, Solomon
TITLE OF INVENTION: Huntingtin-associated protein
FILE REFERENCE: 01107.52271
CURRENT APPLICATION NUMBER: US/08/556.419C
CURRENT FILING DATE: 1995-11-09
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 13
LENGTH: 10348
TYPE: DNA
ORGANISM: Homo sapiens
US-08-556-419-13

Query Match 2.1%; Score 28; DB 3; Length 10348;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 GAGGAGCGCGCGCGCGCGCGCGCG 78
Db 469 GAGGAGCGCGCGCGCGCGCGCGCG 442

RESULT 22
US-09-041-886-14/c
Sequence 14, Application US/09041886
Patent No. 6235872
GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Shartoz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041.886
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 10348 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

FEATURE:
NAME/KEY: CDS
LOCATION: 316..9748
US-09-041-886-14

Query Match 2.1%; Score 28; DB 3; Length 10348;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 GAGGAGCGCGCGCGCGCGCGCGCG 78
Db 469 GAGGAGCGCGCGCGCGCGCGCGCG 442

RESULT 23
US-08-246-982A-5/c
Sequence 5, Application US/08246982A
Patent No. 5686288
GENERAL INFORMATION:
APPLICANT: Macdonald, Marcy E.
APPLICANT: Ambrose, Christine M.
APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246.982A
FILING DATE: May 20, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Joyce, A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609.3880002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10366 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 316..9748
US-08-246-982A-5

Query Match 2.1%; Score 28; DB 2; Length 10366;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 GAGGAGCGCGCGCGCGCGCGCGCG 78
Db 469 GAGGAGCGCGCGCGCGCGCGCGCG 442

RESULT 24
US-08-453-265-5/c
Sequence 5, Application US/08453265
Patent No. 5693757
GENERAL INFORMATION:

APPLICANT: MacDonald, Marcy E.
APPLICANT: Ambrose, Christine M.
APPLICANT: Duyao, Mabel P.
APPLICANT: Gussella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,265
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3880003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10366 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 316..9748
US-08-453-265-5

Query Match 2.1%; Score 28; DB 2; Length 10366;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GAGGAGCGCGCGCGCGCGCGCGCGCG 78
DB 469 GAGGAGCGCGCGCGCGCGCGCGCGCG 442

RESULT 25
US-09-949-016-17589
Sequence 17589, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17589
LENGTH: 43117
TYPE: DNA
ORGANISM: Human
US-09-949-016-17589

Query Match 2.1%; Score 28; DB 3; Length 43117;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 GCGCGCGCGCGCGCGCGCGCGCGGAGCG 83
DB 2083 GCGCGCGCGCGCGCGCGCGCGGAGCG 2110

RESULT 26
US-09-854-133-418
Sequence 418, Application US/09854133
Patent No. 6759508
GENERAL INFORMATION:
APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Raedoh
APPLICANT: Hendersson, Robert A.
APPLICANT: Benson, Darin R.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C10
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 418
LENGTH: 402
TYPE: DNA
ORGANISM: Homo sapiens
US-09-854-133-418

Query Match 2.0%; Score 27; DB 3; Length 402;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 AGGAGGAGCGCGCGCGCGCGCGCGCG 75
DB 186 AGGAGGAGCGCGCGCGCGCGCGCGCG 212

RESULT 27
US-09-949-016-15437/C
Sequence 15437, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15437
LENGTH: 8983
TYPE: DNA
ORGANISM: Human
US-09-949-016-15437

Query Match 2.0%; Score 27; DB 3; Length 8983;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 GCGCGCGCGCGCGCGCGCGCGGAGCG 82


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LENGTH: 641
TYPE: DNA
ORGANISM: Triticum sp.
FEATURE:
NAME/KEY: unsure
LOCATION: (354)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (424)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (482)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (511)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (524)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (528)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (540)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (553)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (556)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (557)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (566)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (568)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (572)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (582)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (601)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (618)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure

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LOCATION: (623)
OTHER INFORMATION: n = a, c, g or t
FEATURE:
NAME/KEY: unsure
LOCATION: (641)
OTHER INFORMATION: n = a, c, g or t
US-09-436-699C-5

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Query Match 2.0%; Score 26; DB 3; Length 641;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 56 GCGCGCGCGCGCGCGCGCGCGCGAGG 81
Db 66 GCGCGCGCGCGCGCGCGCGCGCGAGG 41

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RESULT 33
US-09-436-699C-19/c
Sequence 19, Application US/09436699C
Patent No. 6696619
GENERAL INFORMATION:
APPLICANT: Famodu, Omolayo O.
TITLE OF INVENTION: Plant Aminoacyl-tRNA Synthetases
FILE REFERENCE: B81266 US NA
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: 60/107,276
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 19
LENGTH: 1719
TYPE: DNA
ORGANISM: Triticum aestivum
US-09-436-699C-19

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Query Match 2.0%; Score 26; DB 3; Length 1719;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 56 GCGCGCGCGCGCGCGCGCGCGCGAGG 81
Db 66 GCGCGCGCGCGCGCGCGCGCGCGAGG 41

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RESULT 34
US-09-922-364A-15
Sequence 15, Application US/09922364A
Patent No. 6692937
GENERAL INFORMATION:
APPLICANT: Adelman, John P.
Bond, Chris T.
Maylie, James
Silvia, Christopher P.
TITLE OF INVENTION: Small and Intermediate Conductance,
Calcium-Activated Potassium Channels and Uses
Thereof
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/09/922,364A
FILING DATE: 03-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/254,590
FILING DATE: 10-Mar-1999
APPLICATION NUMBER: US 60/026,451
FILING DATE: 11-SEP-1996
APPLICATION NUMBER: US 60/040,052
FILING DATE: 07-MAR-1997
APPLICATION NUMBER: US 60/045,233
FILING DATE: 17-APR-1997
APPLICATION NUMBER: WO PCT/US97/16033
FILING DATE: 10-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 014210-000730US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1740 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: -
LOCATION: 1..1740
OTHER INFORMATION: /note= "rat small conductance,
calcium-activated potassium channel
protein 2 (rsk2) cDNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-922-364A-15

Query Match 2.0%; Score 26; DB 3; Length 1740;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 GGAGCGCGCGCGCGCGCGCGCG 78
Db 262 GGAGCGCGCGCGCGCGCGCGCG 287

RESULT 35
US-09-254-590-15
Sequence 15, Application US/09254590
Patent No. 6797486
GENERAL INFORMATION:
APPLICANT: Adelman, John P.
Bond, Chris T.
Maylie, James
Silvia, Christopher P.
TITLE OF INVENTION: Small and Intermediate Conductance,
Calcium-Activated Potassium Channels and Uses Thereof
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/254,590
FILING DATE: 10-Mar-1999

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,451
FILING DATE: 11-SEP-1996
APPLICATION NUMBER: US 60/040,052
FILING DATE: 07-MAR-1997
APPLICATION NUMBER: US 60/045,233
FILING DATE: 17-APR-1997
APPLICATION NUMBER: WO PCT/US97/16033
FILING DATE: 10-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 014210-000730US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1740 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: -
LOCATION: 1..1740
OTHER INFORMATION: /note= "rat small conductance,
calcium-activated potassium channel
protein 2 (rsk2) cDNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-254-590-15

Query Match 2.0%; Score 26; DB 3; Length 1740;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 GGAGCGCGCGCGCGCGCGCGCG 78
Db 262 GGAGCGCGCGCGCGCGCGCGCG 287

RESULT 36
US-10-115-415-15
Sequence 15, Application US/10115415
Patent No. 6828122
GENERAL INFORMATION:
APPLICANT: Adelman, John P.
Bond, Chris T.
Maylie, James
Silvia, Christopher P.
TITLE OF INVENTION: Small and Intermediate Conductance,
Calcium-Activated Potassium Channels and Uses
Thereof
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/115,415
FILING DATE: 02-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/254,590

FILING DATE: 10-Mar-1999
APPLICATION NUMBER: US 60/026,451
FILING DATE: 11-SEP-1996
APPLICATION NUMBER: US 60/040,052
FILING DATE: 07-MAR-1997
APPLICATION NUMBER: US 60/045,233
FILING DATE: 17-APR-1997
APPLICATION NUMBER: WO PCT/US97/16033
FILING DATE: 10-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 014210-000730US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1740 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: -
LOCATION: 1..1740
OTHER INFORMATION: /note="rat small conductance,
calcium-activated potassium channel
protein 2 (rsk2) cDNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-115-415-15

Query Match 2.0%; Score 26; DB 3; Length 1740;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 GGAGCGCGCGCGCGCGCGCGCGCG 78
DB 262 GGAGCGCGCGCGCGCGCGCGCG 287

RESULT 37
US-10-116-260-15
Sequence 15, Application US/10116260
Patent No. 6828123
GENERAL INFORMATION:
APPLICANT: Adelman, John P.
Maylie, James
Bond, Chris T.
Silvia, Christopher P.
TITLE OF INVENTION: Small and Intermediate Conductance,
Calcium-Activated Potassium Channels and Uses
Thereof
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/116,260
FILING DATE: 03-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/254,590
FILING DATE: 10-Mar-1999

APPLICATION NUMBER: US 60/026,451
FILING DATE: 11-SEP-1996
APPLICATION NUMBER: US 60/040,052
FILING DATE: 07-MAR-1997
APPLICATION NUMBER: US 60/045,233
FILING DATE: 17-APR-1997
APPLICATION NUMBER: WO PCT/US97/16033
FILING DATE: 10-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 014210-000730US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1740 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: -
LOCATION: 1..1740
OTHER INFORMATION: /note="rat small conductance,
calcium-activated potassium channel
protein 2 (rsk2) cDNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-116-260-15

Query Match 2.0%; Score 26; DB 3; Length 1740;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 GGAGCGCGCGCGCGCGCGCGCGCG 78
DB 262 GGAGCGCGCGCGCGCGCGCGCG 287

RESULT 38
US-10-115-671-15
Sequence 15, Application US/10115671
Patent No. 6828420
GENERAL INFORMATION:
APPLICANT: Adelman, John P.
Maylie, James
Bond, Chris T.
Silvia, Christopher P.
TITLE OF INVENTION: Small and Intermediate Conductance,
Calcium-Activated Potassium Channels and Uses
Thereof
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/115,671
FILING DATE: 03-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/254,590
FILING DATE: 10-Mar-1999
APPLICATION NUMBER: US 60/026,451

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OM nucleic - nucleic search, using sw model

Run on: February 28, 2006, 10:13:56 ; Search time 1202 Seconds
(without alignments)
9088.060 Million cell updates/sec

Title: US-09-934-249-1
Perfect score: 1321
Sequence: 1 cgaccgcgctctcgagcga.....ctgcgtagtgaaagcag 1321

Scoring table: OLIGO.MUC
Gapop 60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

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Minimum DB seq length: 0
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Post-processing: Listing first 500 summaries

Database : Published Applications NA Main:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1321	100.0	1321	3	US-09-934-249-1
2	1229	93.0	4839	6	US-10-241-220-119
3	1229	93.0	4839	6	US-10-269-909-84
4	1229	93.0	4839	6	US-10-269-909-85
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6	1229	93.0	4839	8	US-10-872-991-119
7	1229	93.0	4839	9	US-10-287-436A-300
8	864	65.2	864	6	US-10-295-027-127
9	861	65.2	861	3	US-09-934-249-3
10	860	60.6	1140	6	US-10-390-045-1
11	800	60.6	1140	7	US-10-434-879-1
12	800	60.6	1141	5	US-10-205-823-412
13	800	60.6	1141	6	US-10-301-822-208
14	800	60.6	1141	10	US-11-051-454-412
15	800	60.6	1850	6	US-10-241-220-44
16	800	60.6	1850	8	US-10-872-972-44
17	800	60.6	1850	8	US-10-872-991-44
18	800	60.6	4527	3	US-09-821-812-2
19	800	60.6	4527	8	US-10-849-635-2
20	788	59.7	1066	5	US-10-098-841-71
21	755	57.2	759	6	US-10-390-045-2
22	755	57.2	759	7	US-10-434-879-2
23	749	56.7	969	3	US-09-796-753-55

24	713	54.0	806	6	US-10-241-220-45	Sequence 45, Appl
25	713	54.0	806	8	US-10-872-972-45	Sequence 45, Appl
26	713	54.0	806	8	US-10-872-991-45	Sequence 45, Appl
27	560	42.4	1583	5	US-10-000-266A-32	Sequence 32, Appl
28	401	30.4	408	9	US-10-779-543-11658	Sequence 11658, A
29	302	22.9	693	3	US-09-934-249-14	Sequence 14, Appl
30	178	13.5	1879	9	US-09-918-995-2074	Sequence 2074, Ap
31	106	8.0	368	3	US-10-450-763-20307	Sequence 20307, A
32	102	7.7	368	3	US-09-783-590-3464	Sequence 3464, Ap
33	63	4.8	426	3	US-10-450-763-20306	Sequence 20306, A
34	60	4.5	60	3	US-09-908-975-13620	Sequence 13620, A
35	56	4.2	522	7	US-10-240-425-166	Sequence 166, App
36	50	3.8	65	3	US-09-783-590-3488	Sequence 3488, App
37	45	3.4	837	8	US-10-363-345A-30091	Sequence 30091, A
38	45	3.4	837	8	US-10-363-345A-30092	Sequence 30092, A
39	45	3.4	837	9	US-10-363-483A-30091	Sequence 30091, A
40	44	3.3	878	9	US-09-934-249-12	Sequence 12, Appl
41	44	3.3	1713	3	US-09-934-249-15	Sequence 15, Appl
42	44	3.1	475	3	US-09-934-249-15	Sequence 15, Appl
43	37	2.8	837	8	US-10-363-345A-30089	Sequence 30089, A
44	37	2.8	837	8	US-10-363-483A-30089	Sequence 30089, A
45	37	2.8	837	9	US-10-363-483A-30089	Sequence 30089, A
46	37	2.8	837	9	US-10-363-483A-30090	Sequence 30090, A
47	37	2.8	837	9	US-10-363-483A-30090	Sequence 30090, A
48	34	2.6	555	8	US-10-425-115-66221	Sequence 66221, A
49	34	2.6	640	8	US-10-856-499-146	Sequence 146, App
50	34	2.6	1050	8	US-10-739-930-3690	Sequence 3690, Ap
51	34	2.6	1752	7	US-10-437-963-46088	Sequence 46088, A
52	34	2.6	2000	7	US-10-260-238-2427	Sequence 2427, Ap
53	32	2.4	577	3	US-09-864-761-20542	Sequence 20542, A
54	32	2.4	630	7	US-10-437-963-45057	Sequence 45057, A
55	32	2.4	860	7	US-10-437-963-7883	Sequence 7883, Ap
56	32	2.4	1206	6	US-10-259-165-327	Sequence 327, App
57	32	2.4	1461	7	US-10-767-701-13778	Sequence 13778, A
58	32	2.4	1964	3	US-09-864-761-3776	Sequence 3776, Ap
59	31	2.3	231	7	US-10-437-963-93790	Sequence 93790, A
60	31	2.3	359	8	US-10-856-499-1198	Sequence 1198, Ap
61	31	2.3	533	8	US-10-856-499-1340	Sequence 1340, Ap
62	31	2.3	645	10	US-11-097-143-37082	Sequence 37082, A
63	31	2.3	776	8	US-10-363-345A-19999	Sequence 19999, A
64	31	2.3	776	9	US-10-363-345A-20000	Sequence 20000, A
65	31	2.3	776	9	US-10-363-483A-19999	Sequence 19999, A
66	31	2.3	934	7	US-10-363-483A-20000	Sequence 20000, A
67	31	2.3	934	7	US-10-767-701-9978	Sequence 9278, Ap
68	31	2.3	1295	7	US-10-437-963-11635	Sequence 11635, A
69	31	2.3	2332	6	US-10-104-047-700	Sequence 700, App
70	31	2.3	2808	10	US-11-097-143-37081	Sequence 37081, A
71	30	2.3	427	7	US-10-437-963-28554	Sequence 28554, A
72	30	2.3	918	7	US-10-437-963-28559	Sequence 28559, A
73	30	2.3	1750	7	US-10-437-963-28550	Sequence 28550, A
74	30	2.3	2109	9	US-10-450-763-11281	Sequence 11281, A
75	29	2.2	401	3	US-09-864-761-3536	Sequence 3536, Ap
76	29	2.2	446	3	US-09-864-761-20699	Sequence 20699, A
77	29	2.2	496	7	US-10-767-701-15679	Sequence 15679, A
78	29	2.2	543	7	US-10-437-963-70140	Sequence 70140, A
79	29	2.2	545	8	US-10-363-345A-29381	Sequence 29381, A
80	29	2.2	545	8	US-10-363-345A-29382	Sequence 29382, A
81	29	2.2	545	9	US-10-363-483A-29381	Sequence 29381, A
82	29	2.2	545	9	US-10-363-483A-29382	Sequence 29382, A
83	29	2.2	546	8	US-10-363-345A-12775	Sequence 12775, A
84	29	2.2	546	8	US-10-363-345A-12776	Sequence 12776, A
85	29	2.2	546	9	US-10-363-483A-12775	Sequence 12775, A
86	29	2.2	546	9	US-10-363-483A-12776	Sequence 12776, A
87	29	2.2	546	9	US-10-437-963-54436	Sequence 54436, A
88	29	2.2	739	7	US-10-767-701-4144	Sequence 4144, Ap
89	29	2.2	748	7	US-09-814-351-19603	Sequence 19603, A
90	29	2.2	860	7	US-10-374-780A-1018	Sequence 1018, Ap
91	29	2.2	873	7	US-10-424-599-94182	Sequence 94182, A
92	29	2.2	1128	3	US-09-836-960-1	Sequence 1, Appl
93	29	2.2	1238	7	US-10-437-963-62307	Sequence 62307, A
94	29	2.2	1277	5	US-10-062-254-279	Sequence 279, App
95	29	2.2	1389	7	US-10-437-963-2507	Sequence 2507, Ap
96	29	2.2	1546	6	US-10-393-590-79	Sequence 79, Appl

97	29	2.2	1546	6	US-10-393-567-79	Sequence 79, Appl	170	28	2.1	1371	8	US-10-425-115-135814	Sequence 135814,
98	29	2.2	1546	6	US-10-394-087-79	Sequence 79, Appl	171	28	2.1	1399	7	US-10-437-963-19859	Sequence 19859, A
99	29	2.2	1546	6	US-10-172-118-960	Sequence 960, App	172	28	2.1	1505	7	US-10-437-963-55494	Sequence 55494, A
100	29	2.2	1546	7	US-10-342-887-960	Sequence 960, App	173	28	2.1	1530	8	US-10-425-115-135817	Sequence 135817, A
101	29	2.2	1546	7	US-10-302-812-39	Sequence 39, Appl	174	28	2.1	1766	8	US-10-425-115-94375	Sequence 94375, A
102	29	2.2	1546	7	US-10-848-755A-120	Sequence 120, Appl	175	28	2.1	1784	8	US-10-437-963-88455	Sequence 88455, A
103	29	2.2	1570	3	US-09-836-960-4	Sequence 4, Appl	176	28	2.1	2695	7	US-10-437-963-67083	Sequence 67083, A
104	29	2.2	1835	9	US-10-450-763-14308	Sequence 14308, A	177	28	2.1	4246	7	US-10-755-889-375	Sequence 375, App
105	29	2.2	2253	7	US-10-437-963-17344	Sequence 17344, A	178	28	2.1	9732	9	US-10-450-763-15494	Sequence 15494, A
106	29	2.2	2382	7	US-10-112-944-42	Sequence 42, Appl	179	28	2.1	10348	7	US-10-276-774-427	Sequence 427, App
107	29	2.2	2422	9	US-10-450-763-21135	Sequence 21135, A	180	28	2.1	10348	7	US-10-276-774-490	Sequence 490, App
108	29	2.2	2608	8	US-10-483-029-282	Sequence 282, App	181	28	2.1	10348	9	US-10-419-997-2	Sequence 2, Appl
109	29	2.2	2853	6	US-09-905-983-45	Sequence 45, Appl	182	28	2.1	13672	6	US-10-450-763-27775	Sequence 27775, A
110	29	2.2	2853	6	US-10-177-293-42	Sequence 42, Appl	183	28	2.1	13672	6	US-10-172-118-727	Sequence 727, App
111	29	2.2	2853	7	US-10-778-146-5	Sequence 5, Appl	184	28	2.1	13994	7	US-10-721-693-9	Sequence 9, Appl
112	29	2.2	2987	6	US-10-017-621-89	Sequence 89, Appl	185	28	2.1	13994	7	US-10-852-997-9	Sequence 9, Appl
113	29	2.2	3131	8	US-10-723-860-2262	Sequence 2262, Ap	186	28	2.1	13994	6	US-10-311-455-1114	Sequence 1114, Appl
114	29	2.2	3131	9	US-10-756-149-2088	Sequence 2088, Ap	187	28	2.1	15698	8	US-10-367-094-108	Sequence 108, App
115	29	2.2	3131	9	US-09-814-353-20361	Sequence 20361, A	188	28	2.1	30611	6	US-10-418-182-250	Sequence 250, App
116	29	2.2	3266	3	US-10-293-582-16	Sequence 16, Appl	189	27	2.0	51	7	US-10-418-182-250	Sequence 61426, A
117	29	2.2	3444	6	US-10-805-020-20	Sequence 20, Appl	190	27	2.0	318	9	US-10-437-963-61426	Sequence 61426, A
118	29	2.2	3532	6	US-10-133-937-31	Sequence 31, Appl	191	27	2.0	393	9	US-10-779-543-13119	Sequence 13119, A
119	29	2.2	4122	6	US-10-159-563-31	Sequence 31, Appl	192	27	2.0	402	3	US-09-738-973-418	Sequence 418, App
120	29	2.2	4122	8	US-10-678-160A-13	Sequence 13, Appl	193	27	2.0	402	3	US-09-854-133-418	Sequence 418, App
121	29	2.2	4136	9	US-10-450-763-14307	Sequence 14307, A	194	27	2.0	402	5	US-10-144-649A-418	Sequence 418, App
122	29	2.2	4595	8	US-10-723-860-7451	Sequence 7451, Ap	195	27	2.0	403	7	US-10-767-701-15176	Sequence 15176, A
123	29	2.2	5370	10	US-11-097-143-9056	Sequence 9056, Ap	196	27	2.0	514	8	US-10-363-345A-19053	Sequence 19053, A
124	29	2.2	37966	10	US-11-097-143-9055	Sequence 9055, Ap	197	27	2.0	514	8	US-10-363-345A-19054	Sequence 19054, A
125	29	2.2	53828	7	US-10-322-281-369	Sequence 369, App	198	27	2.0	514	8	US-10-363-483A-19053	Sequence 19053, A
126	29	2.2	1980090	8	US-10-719-993-6815	Sequence 6815, Ap	200	27	2.0	552	4	US-10-363-483A-19054	Sequence 19054, A
127	29	2.2	1980090	8	US-10-741-600-17676	Sequence 17676, A	201	27	2.0	552	4	US-09-925-065A-373740	Sequence 373740, A
128	29	2.1	204	5	US-10-215-432-29	Sequence 29, Appl	202	27	2.0	557	7	US-10-424-599-137788	Sequence 137788, A
129	28	2.1	251	5	US-10-060-036-418	Sequence 418, App	203	27	2.0	581	8	US-10-363-345A-2401	Sequence 2401, Ap
130	28	2.1	293	7	US-10-437-963-57678	Sequence 57678, A	204	27	2.0	581	8	US-10-363-345A-2402	Sequence 2402, Ap
131	28	2.1	321	7	US-10-182-327-163	Sequence 163, App	205	27	2.0	581	9	US-10-363-483A-2401	Sequence 2401, Ap
132	28	2.1	354	7	US-10-437-963-46976	Sequence 46976, A	206	27	2.0	581	9	US-10-363-483A-2402	Sequence 2402, Ap
133	28	2.1	412	3	US-09-960-352-13161	Sequence 13161, A	207	27	2.0	583	4	US-09-925-065A-540849	Sequence 540849, A
134	28	2.1	496	3	US-09-783-590-3813	Sequence 3813, Ap	208	27	2.0	583	4	US-09-925-065A-540850	Sequence 540850, A
135	28	2.1	530	3	US-10-496-129-7	Sequence 7, Appl	209	27	2.0	598	7	US-10-303-165-13	Sequence 13, Appl
136	28	2.1	614	5	US-10-215-433-30	Sequence 30, Appl	210	27	2.0	598	9	US-10-983-197-13	Sequence 13, Appl
137	28	2.1	614	5	US-10-215-433-31	Sequence 31, Appl	211	27	2.0	615	9	US-11-004-765-13	Sequence 13, Appl
138	28	2.1	636	7	US-10-260-238-5871	Sequence 5871, Ap	212	27	2.0	615	9	US-10-487-901-3554	Sequence 3554, Ap
139	28	2.1	729	8	US-10-363-345A-19401	Sequence 19401, A	213	27	2.0	636	7	US-10-437-963-33920	Sequence 33920, A
140	28	2.1	729	8	US-10-363-345A-19402	Sequence 19402, A	214	27	2.0	820	9	US-10-487-901-4656	Sequence 4656, Ap
141	28	2.1	729	9	US-10-363-483A-19401	Sequence 19401, A	215	27	2.0	820	9	US-10-487-901-4656	Sequence 4656, Ap
142	28	2.1	729	9	US-10-363-483A-19402	Sequence 19402, A	216	27	2.0	838	7	US-10-437-963-85737	Sequence 85737, Ap
143	28	2.1	768	8	US-10-389-432B-41	Sequence 41, Appl	217	27	2.0	840	8	US-10-425-115-9262	Sequence 9262, A
144	28	2.1	768	8	US-10-389-432B-47	Sequence 47, Appl	218	27	2.0	849	7	US-10-437-963-17424	Sequence 17424, A
145	28	2.1	771	8	US-10-389-432B-37	Sequence 37, Appl	219	27	2.0	891	7	US-10-437-963-48727	Sequence 48727, A
146	28	2.1	771	8	US-10-389-432B-63	Sequence 63, Appl	220	27	2.0	900	9	US-10-450-763-23585	Sequence 23585, A
147	28	2.1	771	9	US-10-692-367-41	Sequence 41, Appl	221	27	2.0	948	7	US-10-437-963-17422	Sequence 17422, A
148	28	2.1	771	9	US-10-692-367-47	Sequence 47, Appl	222	27	2.0	1041	6	US-10-177-293-285	Sequence 285, App
149	28	2.1	774	8	US-10-389-432B-3	Sequence 3, Appl	223	27	2.0	1119	9	US-10-437-963-85098	Sequence 85098, A
150	28	2.1	774	9	US-10-692-367-7	Sequence 7, Appl	224	27	2.0	1119	9	US-10-481-032A-315	Sequence 315, App
151	28	2.1	774	9	US-10-692-367-37	Sequence 37, Appl	225	27	2.0	1119	9	US-10-481-080-16	Sequence 16, Appl
152	28	2.1	774	9	US-10-692-367-63	Sequence 63, Appl	226	27	2.0	1137	7	US-10-437-963-10547	Sequence 10547, A
153	28	2.1	777	9	US-10-692-367-3	Sequence 3, Appl	227	27	2.0	1137	7	US-10-437-963-10626	Sequence 10626, A
154	28	2.1	816	6	US-10-767-701-13440	Sequence 13440, A	228	27	2.0	1161	7	US-10-303-165-12	Sequence 12, Appl
155	28	2.1	840	6	US-10-259-165-762	Sequence 762, App	229	27	2.0	1161	9	US-10-983-197-12	Sequence 12, Appl
156	28	2.1	845	8	US-10-389-432B-7	Sequence 7, Appl	230	27	2.0	1161	10	US-11-004-765-12	Sequence 12, Appl
157	28	2.1	1061	7	US-10-425-114-15977	Sequence 15977, A	231	27	2.0	1168	7	US-10-425-114-17958	Sequence 17958, A
158	28	2.1	1077	7	US-10-425-114-15467	Sequence 15467, A	232	27	2.0	1197	8	US-10-425-115-6876	Sequence 6876, A
159	28	2.1	1080	5	US-10-215-433-26	Sequence 26, Appl	233	27	2.0	1200	7	US-10-437-963-10546	Sequence 10546, A
160	28	2.1	1080	5	US-10-425-114-23460	Sequence 23460, A	234	27	2.0	1227	7	US-10-437-963-10066	Sequence 10066, A
161	28	2.1	1106	7	US-10-425-114-23406	Sequence 23406, A	235	27	2.0	1285	7	US-10-437-963-38997	Sequence 38997, A
162	28	2.1	1138	7	US-10-425-114-30480	Sequence 30480, A	236	27	2.0	1290	7	US-10-437-963-23855	Sequence 23855, A
163	28	2.1	1144	7	US-10-437-963-85810	Sequence 85810, A	237	27	2.0	1355	7	US-10-437-963-95417	Sequence 95417, A
164	28	2.1	1203	3	US-09-888-370-1	Sequence 1, Appl	238	27	2.0	1403	5	US-10-098-841-280	Sequence 280, App
165	28	2.1	1203	3	US-09-879-312-1	Sequence 1, Appl	239	27	2.0	1416	7	US-10-437-963-33054	Sequence 33054, A
166	28	2.1	1203	3	US-10-923-520-1	Sequence 1, Appl	240	27	2.0	1587	7	US-10-276-774-1315	Sequence 1315, Ap
167	28	2.1	1249	7	US-10-437-963-7575	Sequence 7575, Ap	241	27	2.0	1708	7	US-10-437-963-58654	Sequence 58654, A
168	28	2.1	1249	7	US-10-437-963-95417	Sequence 95417, A	242	27	2.0	1722	7	US-10-437-963-57856	Sequence 57856, A

243	27	2.0	1885	7	US-10-437-963-10100	Sequence 30100, A	316	26	2.0	764	9	US-10-363-483A-16699	Sequence 16699, A
244	27	2.0	1907	7	US-10-437-963-64881	Sequence 64881, A	317	26	2.0	764	9	US-10-363-483A-16700	Sequence 16700, A
245	27	2.0	2031	9	US-10-764-420-948	Sequence 948, App	318	26	2.0	767	7	US-10-260-238-177	Sequence 177, App
246	27	2.0	2424	7	US-10-437-963-62439	Sequence 62439, A	319	26	2.0	772	7	US-10-437-963-64300	Sequence 64300, A
247	27	2.0	2498	6	US-10-094-749-769	Sequence 769, App	320	26	2.0	776	8	US-10-425-115-114213	Sequence 114213, A
248	27	2.0	3110	9	US-10-887-553A-405	Sequence 405, App	321	26	2.0	776	8	US-10-363-445A-4157	Sequence 4157, App
249	27	2.0	3110	9	US-10-734-692-37	Sequence 37, Appl	322	26	2.0	776	9	US-10-363-454A-4158	Sequence 4158, App
250	27	2.0	3110	9	US-10-437-963-37453	Sequence 37453, A	323	26	2.0	777	9	US-10-363-483A-4158	Sequence 4158, App
251	27	2.0	4382	6	US-10-191-997-95	Sequence 95, Appl	324	26	2.0	777	9	US-10-425-114-26543	Sequence 26543, A
252	27	2.0	4767	7	US-10-437-963-93812	Sequence 93812, A	325	26	2.0	821	7	US-10-437-963-71107	Sequence 71107, A
253	27	2.0	154746	3	US-09-827-688-8	Sequence 8, Appl	326	26	2.0	827	7	US-10-437-963-9936	Sequence 9936, App
254	27	2.0	154746	3	US-09-827-688-8	Sequence 8, Appl	327	26	2.0	837	7	US-10-437-963-96070	Sequence 96070, A
255	27	2.0	721377	3	US-10-461-862-163	Sequence 163, App	328	26	2.0	854	8	US-10-363-345A-17765	Sequence 17765, A
256	27	2.0	1711	5	US-10-062-727-5	Sequence 5, Appl	329	26	2.0	854	8	US-10-363-45A-17765	Sequence 17765, A
257	26	2.0	267	7	US-10-062-727-36	Sequence 36, Appl	330	26	2.0	854	9	US-10-363-483A-17765	Sequence 17766, A
258	26	2.0	267	7	US-10-437-963-90333	Sequence 90333, A	331	26	2.0	854	9	US-10-363-483A-17766	Sequence 17767, A
259	26	2.0	276	7	US-10-437-963-89331	Sequence 89331, A	332	26	2.0	854	9	US-10-363-483A-17766	Sequence 17768, A
260	26	2.0	296	7	US-10-437-963-82869	Sequence 82869, A	333	26	2.0	866	7	US-10-437-963-16721	Sequence 16721, A
261	26	2.0	318	5	US-10-062-727-143	Sequence 143, App	334	26	2.0	909	8	US-10-363-45A-14665	Sequence 14665, A
262	26	2.0	367	5	US-10-219-220-2	Sequence 2, Appl	335	26	2.0	909	9	US-10-363-483A-14665	Sequence 14666, A
263	26	2.0	375	3	US-09-867-701-3254	Sequence 3254, App	336	26	2.0	909	9	US-10-363-483A-14666	Sequence 14667, A
264	26	2.0	386	7	US-10-424-599-16581	Sequence 16581, A	337	26	2.0	918	7	US-10-437-963-87734	Sequence 87734, A
265	26	2.0	421	8	US-10-425-115-119786	Sequence 119786, A	338	26	2.0	936	8	US-10-425-115-156161	Sequence 156161, A
266	26	2.0	439	7	US-10-437-963-41638	Sequence 41638, A	339	26	2.0	945	7	US-10-437-963-17374	Sequence 17374, A
267	26	2.0	448	7	US-10-437-963-57458	Sequence 57458, A	340	26	2.0	959	7	US-10-437-963-37082	Sequence 37082, A
268	26	2.0	480	7	US-10-182-243-3	Sequence 3, Appl	341	26	2.0	987	7	US-10-437-963-31927	Sequence 31927, A
269	26	2.0	510	7	US-10-767-701-24141	Sequence 24141, A	342	26	2.0	996	7	US-10-437-963-81564	Sequence 81564, A
270	26	2.0	531	7	US-10-437-963-16296	Sequence 16296, A	343	26	2.0	1040	7	US-10-425-114-12146	Sequence 12146, A
271	26	2.0	538	7	US-10-437-963-43907	Sequence 43907, A	344	26	2.0	1077	9	US-10-450-763-21010	Sequence 21030, A
272	26	2.0	543	6	US-10-029-386-11001	Sequence 11001, A	345	26	2.0	1101	7	US-10-437-963-31633	Sequence 31633, A
273	26	2.0	553	9	US-10-487-901-4768	Sequence 4768, App	346	26	2.0	1121	8	US-10-739-9930-1044	Sequence 5044, App
274	26	2.0	553	9	US-10-487-901-6252	Sequence 6252, App	347	26	2.0	1131	7	US-10-437-963-33755	Sequence 33755, A
275	26	2.0	553	9	US-10-367-057-1118	Sequence 118, App	348	26	2.0	1143	7	US-10-437-963-863	Sequence 863, App
276	26	2.0	564	7	US-10-437-963-61188	Sequence 61188, A	349	26	2.0	1168	8	US-10-363-345A-33621	Sequence 33621, A
277	26	2.0	565	7	US-10-437-963-96947	Sequence 96947, A	350	26	2.0	1168	8	US-10-363-345A-33622	Sequence 33622, A
278	26	2.0	570	7	US-10-374-780A-618	Sequence 618, App	351	26	2.0	1168	9	US-10-363-483A-33621	Sequence 33621, A
279	26	2.0	573	7	US-10-767-701-26095	Sequence 26095, A	352	26	2.0	1168	9	US-10-363-483A-33622	Sequence 33622, A
280	26	2.0	581	8	US-10-363-345A-2471	Sequence 2471, App	353	26	2.0	1175	8	US-10-425-115-11798	Sequence 11798, A
281	26	2.0	581	8	US-10-363-345A-2472	Sequence 2472, App	354	26	2.0	1223	6	US-10-119-428-55	Sequence 55, Appl
282	26	2.0	581	9	US-10-363-483A-2471	Sequence 2471, App	355	26	2.0	1256	8	US-10-363-345A-26539	Sequence 26539, A
283	26	2.0	581	9	US-10-363-483A-2472	Sequence 2472, App	356	26	2.0	1291	8	US-10-363-345A-26540	Sequence 26540, A
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; Publication No. US20030148408A1
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; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillman, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P501081-US
; CURRENT FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 120
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873 AGCGGAGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAG 932
781 AGCGGAGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAG 840
933 AGCGGAGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAG 992
841 AGCGGAGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAG 900
993 GTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1052
901 GTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
1053 TGAAGCGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAG 1112
961 TGAAGCGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAG 1020
1113 AGGTATCGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAG 1172
1021 AGGTATCGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAG 1080

1173 CTTGCTGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAG 1232
1081 CTTGCTGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAG 1140
1233 TCTGAG 1292
1141 TCTGAG 1200
1293 GGGCTGGGAG 1321
1201 GGGCTGGGAG 1229

RESULT 7
US-10-287-436A-300
; Sequence 300, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872.514696
; CURRENT FILING DATE: US/10/287,436A
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FASTSBQ for Windows Version 4.0
; SEQ ID NO 300
; LENGTH: 4839
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-287-436A-300

Query Match 93.0%; Score 1229; DB 9; Length 4839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1229; Conservative 0; Indels 0; Gaps 0;

93 GGAAGCTAGAGGAGAGAGGCTCAAGCCCGGCGGAGAGCGCGCCCGGCTGCGAGCCATT 152
1 GGAAGCTAGAGGAGAGAGGCTCAAGCCCGGCGGAGAGCGCGCCCGGCTGCGAGCCATT 60
153 TTCCGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGG 212
61 TTCCGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGG 120
213 GGGCGAGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAG 272
121 GGGCGAGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAG 180
273 GAGCCGAGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGG 332
181 GAGCCGAGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGG 240
333 CCGAGCTCCGGGCG 392
241 CCGAGCTCCGGGCG 300
393 GCG 452
301 GCG 360
453 CCG 512
361 CCG 420
513 TGGAGATACGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAG 572
421 TGGAGATACGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAG 480
573 TGGAGATACGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAG 632
481 TGGAGATACGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAG 540

[illegible]

```

RESULT 8
US-10-235-027-127
; Sequence 127, Application US/10295027
; Publication No. US2003023350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hwezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666

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	PRIOR FILING DATE: 2001-11-13	
	PRIOR APPLICATION NUMBER: US 60/335,394	
	PRIOR FILING DATE: 2001-11-15	
	PRIOR APPLICATION NUMBER: US 60/332,464	
	PRIOR FILING DATE: 2001-11-21	
	PRIOR APPLICATION NUMBER: US 60/334,393	
	PRIOR FILING DATE: 2001-11-29	
	PRIOR APPLICATION NUMBER: US 60/340,376	
	PRIOR FILING DATE: 2001-12-14	
	PRIOR APPLICATION NUMBER: US 60/347,211	
	PRIOR FILING DATE: 2002-01-08	
	PRIOR APPLICATION NUMBER: US 60/347,349	
	PRIOR FILING DATE: 2002-01-10	
	PRIOR APPLICATION NUMBER: US 60/355,250	
	PRIOR FILING DATE: 2002-02-08	
	PRIOR APPLICATION NUMBER: US 60/356,714	
	PRIOR FILING DATE: 2002-02-13	
	Remaining Prior Application data removed - See File Wrapper or PALM.	
	NUMBER OF SEQ ID NOS: 1386	
	SOFTWARE: PatentIn Ver. 2.1	
	SEQ ID NO 127	
	LENGTH: 864	
	TYPE: DNA	
	ORGANISM: Homo sapiens	
	US-10-295-027-127	
Query Match	65.4%; Score 864; DB 6; Length 864;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 864; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Df	413 ATGACCGCTTGATGGGGGTCAAGCAGCACGCCGCGCCGCGCGCGGAGCCCATGTC	472
	1 ATGCACCGCTTGATGGGGGTAAACAGCACGCCGCGCGCGCGCGGAGCCCATGTC	60
Df	473 TCCTGCACTGTCACA CTGCAACGCTCTTTTGTTCAGACATGAGATCACGAGCTGGAG	532
	61 TCTGCACTGTCACA CTGCAACGCTCTTTTGTTCAGACATGAGATCACGAGCTGGAG	120
Df	533 TTGTGTCATCATCATCATCTGTGTGTGTATGATGTGATGTGTGTGTATCATCTGTC	592
	121 TTTGTTCAATCATCATCATCATGTGTGTGTGTATGATGTGATGTGTGTATCATCTGTC	180
Df	593 CTGCTGAGCCACTCAAGCTGTCTGCAAGGCTTTCATCAGCGGACAGCGAGGGCGG	652
	181 CTGCTGACCCTACAGCTGTCTGTGACAGTCTTTCATCAGCCGAGCACAGCGAGGGCGG	240
Df	653 AGGAGAGAAGATGCCCCCTGTCTCAAGAGATGCTGTGGCCCTCGAGAGCAGATGTCA	712
	241 AGGAGAGAAGATGCCCCCTGTCTCAAGAGATGCTGTGGCCCTCGAGAGCAGATGTCA	300
Df	713 GGCAACGGAATCCAGAGCGCAGAGTCTTAGCGCCCGCTCGGCCCACCGACCGCTGGCC	772
	301 GGCAACGGAATCCAGAGCGCAGAGTCTTAGCGCCCGCTCGGCCCACCGACCGCTGGCC	360
Df	773 GTGCGCCCTTCGCGCAGCGGAGGCTTTCACCGCTTCAGCCCACTTATCCGATCTG	832
	361 GTGCGCCCTTCGCGCAGCGGAGGCTTTCACCGCTTCAGCCCACTTATCCGATCTG	420
Df	833 CAGCACGAGATCGA CTTGCAACCACTCTGCTGTCAAGCGGAGAGAACCCCACTCC	892
	421 CAGCACGAGATCGA CTTGCAACCACTCTGCTGTCAAGCGGAGAGAACCCCACTCC	480
Df	893 TACCAAGGCGCCCTGCA CCGCTTCAGCTTGTGGAGCCCGAGCAGAGCTGGAATGAACCGG	952
	481 TACCAAGGCGCCCTGCA CCGCTTCAGCTTGTGGAGCCCGAGCAGAGCTGGAATGAACCGG	540
Df	953 GAGTGTGTGTGCGGCA CCCCCCAAAGAACATTTTCCAATTGACCTGATGATGATGTC	1012
	541 GAGTGTGTGTGCGGCA CCCCCCAAAGAACATTTTCCAATTGACCTGATGATGATGTC	600
Df	1013 AGGCTGGGCGGCGCCCTGCGCCCGCCAGAGTAATCTGGGACATCAGCGCAGCTGTCA CGC	1072
	601 AGGCTGGGCGGCGCCCTGCGCCCGCCAGAGTAATCTGGGACATCAGCGCAGCTGTCA CGC	660

Db	100	CGGAGCTGAGGATTTGTTTCAGATCAATCAATCAATCGTGTGTGTGATGATGAGTGATGTGTGTGG	159
Qy	582	TGATCACTGTGCTGTGCTGATGCCATCAACAGCTGTGTGCACTGTCTTCAATCAGCTGGCAGCA	641
Db	160	TGATCACTGTGCTGTGCTGATGCCATCAACAGCTGTGTGCACTGTCTTCAATCAGCTGGCAGCA	219
Qy	642	GCCAGGGGGCCGAGGAGAGAAATGATGCCCTGTCTCTAGAAAGAAATGCTGTGGGCGCTTCGGAGA	701
Db	220	GCCAGGGGGCCGAGGAGAGAAATGATGCCCTGTCTCTAGAAAGAAATGCTGTGGGCGCTTCGGAGA	279
Qy	702	GCAcAGTGTcAGGcAAcCGAAATCCcAGAcCGGcAGcTcAGcTcAGcCCcCGcCTTCGGcCCAcCG	761
Db	280	GCAcAGTGTcAGGcAAcCGAAATCCcAGAcCGGcAGcTcAGcCCcCGcCTTCGGcCCAcCG	339
Qy	762	ACCcGCTGTGcCGGTcCGcCGCTTCCTTcCGcCCcAGcGGGAGcGCTTCcACAcCGCTTCcAGcCCAcCT	821
Db	340	ACCcGCTGTGcCGGTcCGcCGCTTCCTTcCGcCCcAGcGGGAGcGCTTCcACAcCGCTTCcAGcCCAcCT	399
Qy	822	ATTCGATcCTGTGcAGAcCGAGATTCGAcCTTCGcAGcCCAcCCAcCCAcCATCTcGTGTcAGAcCGGGAGG	881
Db	400	ATTCGATcCTGTGcAGAcCGAGATTCGAcCTTCGcAGcCCAcCCAcCCAcCATCTcGTGTcAGAcCGGGAGG	459
Qy	882	AGcCCcCCAcCCCTTAcCCAGGcCCcCTGTcACAcCTTCAGcTTCGGGAcCCcCGcAGcAGcAGCTGTG	941
Db	460	AGcCCcCCAcCCCTTAcCCAGGcCCcCTGTcACAcCTTCAGcTTCGGGAcCCcCGcAGcAGcAGCTGTG	519
Qy	942	AACTGAAcCCGGGAGTcCGGTGTGcGGcGcAcCCcCCcAAAcGAAcCATCTTcGAcAGcGTAcCTGTGA	1001
Db	520	AACTGAAcCCGGGAGTcCGGTGTGcGGcGcAcCCcCCcAAAcGAAcCATCTTcGAcAGcGTAcCTGTGA	579
Qy	1002	TGGAATGAGcCAGGcCTGTGGcCGGcCCcCTGTcCCcCCcCAGcAGcATAcCTcCGGgAcCTAcAGcCGcCA	1061
Db	580	TGGAATGAGcCAGGcCTGTGGcCGGcCCcCTGTcCCcCCcCAGcAGcATAcCTcCGGgAcCTAcAGcCGcCA	639
Qy	1062	CGTGTcTAcCGGcAGcCGGcCGGcCGcCATGTAGAGGGgCGcCGcCCAcCTTAcAGcCGAGcGTcATcCG	1121
Db	640	CGTGTcTAcCGGcAGcCGGcCGGcCGcCATGTAGAGGGgCGcCGcCCAcCTTAcAGcCGAGcGTcATcCG	699
Qy	1122	GCCAcTAcCCcCGGGgGTcCTcCTTTCAGAcGAcCAGAcAGAcAGAcGTGGcCGGcCCcCTTCCTTGGcTG	1181
Db	700	GCCAcTAcCCcCGGGgGTcCTcCTTTCAGAcGAcCAGAcAGAcAGAcGTGGcCGGcCCcCTTCCTTGGcTG	759
Qy	1182	AGGGGAcCCcGGcCTCCAcCAGcAcAcAcATcCGGcCCcCTTcGAGAcGcGcAcCCAcCTTcGAGcCA	1241
Db	760	AGGGGAcCCcGGcCTCCAcCAGcAcAcAcATcCGGcCCcCTTcGAGAcGcGcAcCCAcCTTcGAGcCA	819
Qy	1242	AAAGAAAGATTAACAGAAAGGAcAcCCCTCTTcTAGGgGTCCcCAGGGgGGcCTGGgCTGTGGGg	1301
Db	820	AAAGAAAGATTAACAGAAAGGAcAcCCCTCTTcTAGGgGTCCcCAGGGgGGcCTGGgCTGTGGGg	879
Qy	1302	CTGcCTAcGTGTGAAGGcAG	1321
Db	880	CTGcCTAcGTGTGAAGGcAG	899

```

RESULT 14
US-11-051-454-412
: Sequence 412, Application US/11051454
: Publication No. US20050191673A1
GENERAL INFORMATION:
: APPLICANT: Schlegel, Robert
: APPLICANT: Monahan, John E.
: APPLICANT: Endege, Wilson O.
: APPLICANT: Gannavarapu, Manjula
: APPLICANT: Goratcheva, Bella
: APPLICANT: Hoersch, Sebastian
: APPLICANT: Kamatkar, Shubhangi
: APPLICANT: Monsey, Angela M.
: APPLICANT: Glatc, Karen
: APPLICANT: Zhao, Xumei
: APPLICANT: Anderson, Duetlin
: TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
: TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND

```

[illegible]

Db 760 AGGGACCCGGCTCCACACACACATCGCCCTTAGAGAGCGACCATCTGAGCA 819
Qy 1242 AAGAGAGATTAACAGAAAGACACCTCTCTAGGGTCCCAAGGGGCGCGGCTGAG 1301
Db 820 AAGAGAGATTAACAGAAAGACACCTCTCTAGGGTCCCAAGGGGCGCGGCTGAG 879
Qy 1302 CTGCGTAGTGAAAAAGGCAG 1321
Db 880 CTGCGTAGTGAAAAAGGCAG 899

RESULT 15
US-10-241-220-44

Sequence 44, Application US/10241220
Publication No. US20030148408A1
GENERAL INFORMATION:
APPLICANT: Frantz, Gretchen
APPLICANT: Hillan, Kenneth J.
APPLICANT: Phillips, Heidi
APPLICANT: Polakis, Paul
APPLICANT: Spencer, Susan
APPLICANT: Williams, P. Mickey
APPLICANT: Wu, Thomas
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TREATMENT OF TUMOR
FILE REFERENCE: P5010R1-US
CURRENT APPLICATION NUMBER: US/10/241,220
CURRENT FILING DATE: 2002-12-13
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 44
LENGTH: 1850
TYPE: DNA
ORGANISM: Homo Sapien
US-10-241-220-44

Query Match 60.6%; Score 800; DB 6; Length 1850;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 800; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 522 CGAGCTGAGTTTGTTCAGATCATCATCTGCTGATATGATGATGATGATG 581
Db 100 CGAGCTGAGTTTGTTCAGATCATCATCTGCTGATATGATGATGATGATG 159
Qy 582 TGATCAGTGTCTGAGGCACTCAAGCTGTGACAGGCTTTCATCAGCGGACCA 641
Db 160 TGATCAGTGTCTGAGGCACTCAAGCTGTGACAGGCTTTCATCAGCGGACCA 219
Qy 642 GCCAGGGCGAGAGAGAGATGCTGTCTCAGAAAGATGCTGTGCTCGAGA 701
Db 220 GCCAGGGCGAGAGAGATGCTGTCTCAGAAAGATGCTGTGCTCGAGA 279
Qy 702 GCACAGTGTCAAGCAAGAAATCCAGAGCCGCAAGTCTAGCCGCCCTCGGACCA 761
Db 280 GCACAGTGTCAAGCAAGAAATCCAGAGCCGCAAGTCTAGCCGCCCTCGGACCA 339
Qy 762 ACCGCTGGCGGTGCGCCCTTGCCAGCGGAGGCGCTTCCAGCGCTTCCAGCCCACT 821
Db 340 ACCGCTGGCGGTGCGCCCTTGCCAGCGGAGGCGCTTCCAGCGCTTCCAGCCCACT 399
Qy 822 ATCCGTACTGACGACGAGATGACCTGCAACCCACCATCTCGTGTGACAGGGAGG 881
Db 400 ATCCGTACTGACGACGAGATGACCTGCAACCCACCATCTCGTGTGACAGGGAGG 459
Qy 882 AGCCCCACCTTACCAAGGCGCCCTTGCACTTGGGAGCCCGAGCAGAGCTGG 941
Db 460 AGCCCCACCTTACCAAGGCGCCCTTGCACTTGGGAGCCCGAGCAGAGCTGG 519
Qy 942 AACTGAACCGGAGTGTGAGCGGACCCCAAAAGAAACATCTTTCAGACATGACTGA 1001
Db 520 AACTGAACCGGAGTGTGAGCGGACCCCAAAAGAAACATCTTTCAGACATGACTGA 579

Qy 1002 TGGATAGTGCAGAGTGTGAGCGGCGCCCTGACCCCAAGCACTAACTCGGGGACATGAGCCCA 1061
Db 580 TGGATAGTGCAGAGTGTGAGCGGCGCCCTGACCCCAAGCACTAACTCGGGGACATGAGCCCA 639
Qy 1062 CGTGCTACGAGCAGCGGCGGCGCATGAGAGGGGCGCGCCCACTTACAGGAGTCACTG 1121
Db 640 CGTGCTACGAGCAGCGGCGGCGCATGAGAGGGGCGCGCCCACTTACAGGAGTCACTG 699
Qy 1122 GCCACTACCGGGGCTCTCTTCCAGACACGAGAGCAGTGGAGCGCCCTCTGCTGG 1181
Db 700 GCCACTACCGGGGCTCTCTTCCAGACACGAGAGCAGTGGAGCGCCCTCTGCTGG 759
Qy 1182 AGGGACCCGGCTCCACACACACATCGGCGCCCTTAGAGAGCGACCATCTGAGCA 1241
Db 760 AGGGACCCGGCTCCACACACACATCGGCGCCCTTAGAGAGCGACCATCTGAGCA 819
Qy 1242 AAGAGAGATTAACAGAAAGACACCTCTCTAGGGTCCCAAGGGGCGCGGCTGAG 1301
Db 820 AAGAGAGATTAACAGAAAGACACCTCTCTAGGGTCCCAAGGGGCGCGGCTGAG 879
Qy 1302 CTGCGTAGTGAAAAAGGCAG 1321
Db 880 CTGCGTAGTGAAAAAGGCAG 899

RESULT 16
US-10-872-972-44

Sequence 44, Application US/10872972
Publication No. US20040229277A1
GENERAL INFORMATION:
APPLICANT: Frantz, Gretchen
APPLICANT: Hillan, Kenneth J.
APPLICANT: Phillips, Heidi
APPLICANT: Polakis, Paul
APPLICANT: Spencer, Susan
APPLICANT: Williams, P. Mickey
APPLICANT: Wu, Thomas
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TREATMENT OF TUMOR
FILE REFERENCE: P5010R1-US
CURRENT APPLICATION NUMBER: US/10/872,972
CURRENT FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US/10/241,220
PRIOR FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 44
LENGTH: 1850
TYPE: DNA
ORGANISM: Homo Sapien
US-10-872-972-44

Query Match 60.6%; Score 800; DB 8; Length 1850;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 800; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 522 CGAGCTGAGTTTGTTCAGATCATCATCTGCTGATATGATGATGATGATG 581
Db 100 CGAGCTGAGTTTGTTCAGATCATCATCTGCTGATATGATGATGATGATG 159
Qy 582 TGATCAGTGTCTGAGGCACTCAAGCTGTGACAGGCTTTCATCAGCGGACCA 641
Db 160 TGATCAGTGTCTGAGGCACTCAAGCTGTGACAGGCTTTCATCAGCGGACCA 219
Qy 642 GCCAGGGCGAGAGAGATGCTGTCTCAGAAAGATGCTGTGCTCGAGA 701
Db 220 GCCAGGGCGAGAGAGATGCTGTCTCAGAAAGATGCTGTGCTCGAGA 279
Qy 702 GCACAGTGTCAAGCAAGAAATCCAGAGCCGCAAGTCTTACAGCGGACCA 761
Db 280 GCACAGTGTCAAGCAAGAAATCCAGAGCCGCAAGTCTTACAGCGGACCA 339
Qy 762 ACCGCTGGCGGTGCGCCCTTGCCAGCGGAGGCGCTTCCAGCGCTTCCAGCCCACT 821

	Matches	763;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	522	CGAGCTGGAGATTGTTTCAGATCATCATCATCTGTGTGTGTATGTATGTGTATGTGTGTGTG								581
Db	37	CGAGCTGGAGATTGTTTCAGATCATCATCATCTGTGTGTGTATGTATGTGTATGTGTGTGTG								96
QY	582	TGATCACTGTGCTGTGTGACCACTTCAAGAGCTGTCTGTGCAAGGCTCTTCAATCAAGCCGGACAA								641
Db	97	TGATCACTGTGCTGTGTGACCACTTCAAGAGCTGTCTGTGCAAGGCTCTTCAATCAAGCCGGACAA								156
QY	642	GCCAGGGGCGAGGAGAGAGATGCTGTCTGTCTTCAAGAGATGCTCTGTGCGCTTGGAGCA								701
Db	157	GCCAGGGGCGAGGAGAGAGATGCTGTCTGTCTTCAAGAGATGCTCTGTGCGCTTGGAGCA								216
QY	702	GCACAGTGTCAAGGCAACGGAATCCAGAGCCGAGAGCTTACGCCCCCTGTGAGCCACCG								761
Db	217	GCACAGTGTCAAGGCAACGGAATCCAGAGCCGAGAGCTTACGCCCCCTGTGAGCCACCG								276
QY	762	ACCGCTGTGGCGGTGCGCGCTTGGCGGAGCGGCTTCCACCGCTTCCAGCCACT								821
Db	277	ACCGCTGTGGCGGTGCGCGCTTGGCGGAGCGGCTTCCACCGCTTCCAGCCACT								336
QY	822	ATCCGTCCTTCAGACAGAGATTCAGCTTGCACCCAGCATCTCGCTGTCAAGCGGGAGG								881
Db	337	ATCCGTCCTTCAGACAGAGATTCAGCTTGCACCCAGCATCTCGCTGTCAAGCGGGAGG								396
QY	882	AGCCCCACCCCTTACCGAGGGGCCCTTGCACCTTCAGCTTGTGGAGCCCGGAGCGAGCTGG								941
Db	397	AGCCCCACCCCTTACCGAGGGGCCCTTGCACCTTCAGCTTGTGGAGCCCGGAGCGAGCTGG								456
QY	942	AACTGAACCCGGAGATCGGTGTGGCGGCACCCCGAAACGAACCATCTTTCAGACATGACTGGA								1001
Db	457	AACTGAACCCGGAGATCGGTGTGGCGGCACCCCGAAACGAACCATCTTTCAGACATGACTGGA								516
QY	1002	TGATATGTGCCAGAGCTGTGGGCGGCGCCCTGCGCCCCGAGAGTAACTCGGGCATCAAGCGCA								1061
Db	517	TGATATGTGCCAGAGCTGTGGGCGGCGCCCTGCGCCCCGAGAGTAACTCGGGCATCAAGCGCA								576
QY	1062	CGTGTACCGGCGAGCGGCGGCGCATGAGAGGGCGCGCGCCACCTTACAGCGAGGTGATCG								1122
Db	577	CGTGTACCGGCGAGCGGCGGCGCATGAGAGGGCGCGCGCCACCTTACAGCGAGGTGATCG								636
QY	1122	GCCACTACCCGGGGTCTCTTTCAGACACACAGACAGAGTGGGCGCCCTCTCTTGTGTGG								1181
Db	637	GCCACTACCCGGGGTCTCTTTCAGACACACAGACAGAGTGGGCGCGCCCTCTTGTGTGG								696
QY	1182	AGGGGACCCGGCTCCACACACACACATCGGGCGCCCTTACAGAGCGAGCATCTGGAGCA								1241
Db	697	AGGGGACCCGGCTCCACACACACACATCGGGCGCCCTTACAGAGCGAGCATCTGGAGCA								756
QY	1242	AAGAGAGGATTAACAGAAAGGACACCTCTCTAGGGTCCCGAG								1285
Db	757	AAGAGAGGATTAACAGAAAGGACACCTCTCTAGGGTCCCGAG								800
RESULT 25										
US-10-872-972-45										
; Sequence 45, Application US/10872972										
; Publication No. US20040229277A1										
; GENERAL INFORMATION:										
; APPLICANT: Frantz, Gretchen										
; APPLICANT: Hillan, Kenneth J.										
; APPLICANT: Phillips, Heidi										
; APPLICANT: Polakis, Paul										
; APPLICANT: Spencer, Susan										
; APPLICANT: Williams, P. Mickey										
; APPLICANT: Wu, Thomas										
; APPLICANT: Zhang, Zemin										
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND										
; TITLE										

```

; PRIOR APPLICATION NUMBER: US/10/241,220
; PRIOR FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 45
; LENGTH: 806
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-872-972-45

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Query Match	54.0%	Score 713;	DB 8;	Length 806;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 763; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0

[illegible]


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US-10-779-543-11658
; Sequence 11658, Application US/10779543
; Publication No. US2005022791A1
;
; GENERAL INFORMATION:
; APPLICANT: Williams et al
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
; TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
; FILE REFERENCE: 2300-21302
; CURRENT APPLICATION NUMBER: US/10/779,543
; CURRENT FILING DATE: 2004-02-12
;
; PRIOR APPLICATION NUMBER: 10/076,555
; PRIOR FILING DATE: 2002-02-15
;
; PRIOR APPLICATION NUMBER: 09/217,471
; PRIOR FILING DATE: 1998-12-21
;
; PRIOR APPLICATION NUMBER: 60/066,755
; PRIOR FILING DATE: 1997-12-23
;
; PRIOR APPLICATION NUMBER: 60/080,664
; PRIOR FILING DATE: 1998-04-03
;
; PRIOR APPLICATION NUMBER: 60/105,234
; PRIOR FILING DATE: 1998-10-21
;
; PRIOR APPLICATION NUMBER: 09/297,648
; PRIOR FILING DATE: 2000-04-10
;
; PRIOR APPLICATION NUMBER: PCT/US99/01619
; PRIOR FILING DATE: 1999-01-28
;
; PRIOR APPLICATION NUMBER: 60/072,910
; PRIOR FILING DATE: 1998-01-28
;
; PRIOR APPLICATION NUMBER: 60/075,954
; PRIOR FILING DATE: 1998-02-24
;
; PRIOR APPLICATION NUMBER: 60/080,114
; PRIOR FILING DATE: 1998-03-31
;
; Remaining Prior Application data removed - See File Wrapper or PALM
; NUMBER OF SEQ ID NOS: 23767
;
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11658
;
; LENGTH: 408
; TYPE: DNA
;
; ORGANISM: Homo sapiens
US-10-779-543-11658

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LENGTH: 467
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(467)
OTHER INFORMATION: n = A,T,C or G
US-09-918-995-2074

Query Match 13.5%; Score 178; DB 3; Length 467;
Best Local Similarity 100.0%; Pred. No. 3.9e-77;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1144 CCAGACAGCAGACAGACAGTGGGGCGCCCTCTGCTGAGAGGGAGACCGGCTCCACCAAC 1203
DB 36 CCAGACAGCAGCAGACAGTGGGGCGCCCTCTGCTGAGAGGGAGACCGGCTCCACCAAC 95
QY 1204 ACACATCGCGCCCTAGAGAGCGCAGCCATCTGAGCAAGAGATTAACAGAAAG 1263
DB 96 ACACATCGCGCCCTAGAGAGCGCAGCCATCTGAGCAAGAGATTAACAGAAAG 155
QY 1264 ACACCTCTCTAGGGTCCCAAGGGGGCGGGCTGGGCTGGTGAAGAGGAG 1321
DB 156 ACACCTCTCTAGGGTCCCAAGGGGGCGGGCTGGGCTGGTGAAGAGGAG 213

RESULT 31
US-10-450-763-20307

; Sequence 20307, Application US/10450763
; Publication No. US20050196754A1

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc

; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

; FILE REFERENCE: 790CIP3/US

; CURRENT APPLICATION NUMBER: US/10/450,763

; CURRENT FILING DATE: 2003-06-11

; PRIOR APPLICATION NUMBER: PCT/US01/08631

; PRIOR FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: 09/540,217

; PRIOR FILING DATE: 2000-03-31

; PRIOR APPLICATION NUMBER: 09/649,167

; PRIOR FILING DATE: 2000-08-23

; NUMBER OF SEQ ID NOS: 60736

; SOFTWARE: Custom

; SEQ ID NO: 20307

; LENGTH: 1879

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SIMILAR

; LOCATION: (473)...(835)

; OTHER INFORMATION: 32% homologous to Homo sapiens dU7187.1 (PMEPA1 protein (an

; OTHER INFORMATION: androgen induced type 1b transmembrane protein)., accession numbe

; US-10-450-763-20307

Query Match 8.0%; Score 106; DB 9; Length 1879;
Best Local Similarity 100.0%; Pred. No. 1e-41;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 788 CAGCGGAGCGCTTCCACCGCTTCCAGCCACCTATCTGCTGAGAGAGATTCAGC 847
DB 333 CAGCGGAGCGCTTCCACCGCTTCCAGCCACCTATCTGCTGAGAGAGATTCAGC 392
QY 848 CTGCCACCCACCATCTGCTGTCAAGCGGGAGAGACCCCAACCT 893
DB 393 CTGCCACCCACCATCTGCTGTCAAGCGGGAGAGACCCCAACCT 438

RESULT 32
US-09-783-590-3464
; Sequence 3464, Application US/09783590
; Patent No. US20020110850A1

; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.

; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16-2C1

; CURRENT APPLICATION NUMBER: US/09/783,590

; CURRENT FILING DATE: 2000-02-15

; PRIOR APPLICATION NUMBER: 08/420,856

; PRIOR FILING DATE: 1995-04-12

; PRIOR APPLICATION NUMBER: 08/346,731

; PRIOR FILING DATE: 1994-11-21

; NUMBER OF SEQ ID NOS: 12485

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3464

; LENGTH: 368

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (103)

; OTHER INFORMATION: n equals a,t,g, or c

; NAME/KEY: misc_feature

; LOCATION: (825)

; OTHER INFORMATION: n equals a,t,g, or c

; NAME/KEY: misc_feature

; LOCATION: (279)

; OTHER INFORMATION: n equals a,t,g, or c

; NAME/KEY: misc_feature

; LOCATION: (314)

; OTHER INFORMATION: n equals a,t,g, or c

; NAME/KEY: misc_feature

; LOCATION: (349)

; OTHER INFORMATION: n equals a,t,g, or c

; NAME/KEY: misc_feature

; LOCATION: (350)

; OTHER INFORMATION: n equals a,t,g, or c

; NAME/KEY: misc_feature

; LOCATION: (366)

; OTHER INFORMATION: n equals a,t,g, or c

; NAME/KEY: misc_feature

; LOCATION: (367)

; OTHER INFORMATION: n equals a,t,g, or c

; NAME/KEY: misc_feature

; LOCATION: (368)

; OTHER INFORMATION: n equals a,t,g, or c

; US-09-783-590-3464

Query Match 7.7%; Score 102; DB 3; Length 368;
Best Local Similarity 100.0%; Pred. No. 1.2e-39;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1127 TACCGGGGTCCTCTTCCAGACACAGCAGTGGGCGCCCTCTGCTGAGAGG 1186
DB 1 TACCGGGGTCCTCTTCCAGACACAGCAGTGGGCGCCCTCTGCTGAGAGG 60
QY 1187 ACCCGGCTCCACACACACACATCGGCCCTCTAGAGAGCGCA 1228
DB 61 ACCCGGCTCCACACACACACATCGGCCCTCTAGAGAGCGCA 102

RESULT 33
US-10-450-763-20306
; Sequence 20306, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11


```
;; PRIOR APPLICATION NUMBER: PCT/US01/08631
;; PRIOR FILING DATE: 2001-03-30
;; PRIOR APPLICATION NUMBER: 09/540,217
;; PRIOR FILING DATE: 2000-03-31
;; PRIOR APPLICATION NUMBER: 09/649,167
;; PRIOR FILING DATE: 2000-08-23
;; NUMBER OF SEQ ID NOS: 60736
;; SOFTWARE: Custom
;; SEQ ID NO 20306
;; LENGTH: 426
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SIMILAR
;; LOCATION: (13)..(57)
;; OTHER INFORMATION: 93% homologous to Homo sapiens d718j7.1 (PMEP1 protein (an
;; OTHER INFORMATION: androgen induced type 1b transmembrane protein)), accession numbe
;; OTHER INFORMATION: AL035541, Smith-Waterman Score=79.
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(426)
;; OTHER INFORMATION: n = a,t,c or g
US-10-450-763-20306
```

```
Query Match          4.8%; Score 63; DB 9; Length 426;
Best Local Similarity 100.0%; Pred. No. 2e-20;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1259 AAGAGCACCCTCTCTAGGGGTCGCCAGGGGCGGGGCTGCGGAGTGAAGG 1318
DB      43 AAGAGCACCCTCTCTAGGGGTCGCCAGGGGCGGGGCTGCGGAGTGAAGG 102
```

```
QY      1319 CAG 1321
DB      103 CAG 105
```

```
RESULT 34
US-09-908-975-13620
;; Sequence 13620, Application US/09908975
;; Publication No. US20030165843A1
;; GENERAL INFORMATION:
;; APPLICANT: SHOSHAN, Avi
;; APPLICANT: WASSERMAN, Alon
;; APPLICANT: MINTZ, Eli
;; APPLICANT: MINTZ, Liat
;; APPLICANT: FAIGER, Simcha
;; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
;; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
;; FILE REFERENCE: 36688-0005
;; CURRENT APPLICATION NUMBER: US/09/908,975
;; PRIOR FILING DATE: 2001-07-20
;; PRIOR APPLICATION NUMBER: US 60/287,724
;; PRIOR FILING DATE: 2001-05-02
;; PRIOR APPLICATION NUMBER: US 60/221,607
;; PRIOR FILING DATE: 2000-07-28
;; NUMBER OF SEQ ID NOS: 32337
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 13620
;; LENGTH: 60
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-908-975-13620
```

```
Query Match          4.5%; Score 60; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 8.3e-19;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1225 CGAGGCATCTGAGCAAGAGTAAGCAAGGACCCCTCTCTAGGGTCCCA 1284
DB      1 CGAGGCATCTGAGCAAGAGTAAGCAAGGACCCCTCTCTAGGGTCCCA 60
```

```
RESULT 35
US-10-240-425-166
;; Sequence 166, Application US/10240425
;; Publication No. US2004003502A1
;; GENERAL INFORMATION:
;; APPLICANT: Williams, Amanda
;; APPLICANT: Boland, Joseph F.
;; APPLICANT: Lord, Reginald V.
;; APPLICANT: Alvarez, Chris
;; APPLICANT: Wetzel, Jon C.
;; APPLICANT: Scheer, Uwe
;; APPLICANT: Vockley, Joseph G.
;; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
;; FILE REFERENCE: 44921-5026
;; CURRENT APPLICATION NUMBER: US/10/240,425
;; PRIOR FILING DATE: 2002-09-30
;; PRIOR APPLICATION NUMBER: PCT/US01/09847
;; PRIOR FILING DATE: 2001-03-28
;; PRIOR APPLICATION NUMBER: US 60/193,446
;; PRIOR FILING DATE: 2000-03-31
;; NUMBER OF SEQ ID NOS: 1588
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 166
;; LENGTH: 522
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: Genbank Accession No. US2004003502A1 AA35819
US-10-240-425-166
```

```
Query Match          4.2%; Score 56; DB 7; Length 522;
Best Local Similarity 100.0%; Pred. No. 5.5e-17;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1234 CTGAGCAAGAGAGATTAACAGAAAGACACCTCTCTAGGGTCCCGAGGGG 1289
DB      36 CTGAGCAAGAGAGATTAACAGAAAGACACCTCTCTAGGGTCCCGAGGGG 91
```

```
RESULT 36
US-09-783-590-3488
;; Sequence 3488, Application US/09783590
;; Patent No. US20020110850A1
;; GENERAL INFORMATION:
;; APPLICANT: Dillon, Patrick J.
;; APPLICANT: Haseltine, William A.
;; APPLICANT: Li, Haodong
;; APPLICANT: Rosen, Craig A.
;; APPLICANT: Ruben, Steven M.
;; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
;; FILE REFERENCE: PO-16,2C1
;; CURRENT APPLICATION NUMBER: US/09/783,590
;; PRIOR FILING DATE: 2000-02-15
;; PRIOR APPLICATION NUMBER: 08/420,856
;; PRIOR FILING DATE: 1995-04-12
;; PRIOR APPLICATION NUMBER: 08/346,731
;; PRIOR FILING DATE: 1994-11-21
;; NUMBER OF SEQ ID NOS: 12485
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 3488
;; LENGTH: 65
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (51)
;; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-3488
```

```
Query Match          3.8%; Score 50; DB 3; Length 65;
Best Local Similarity 100.0%; Pred. No. 7e-14;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



```
Oy 1127 TACCGGGGTCTCTTCCAGACAGAGAGAGAGGCGGCGCTCTT 1176
|||
Db 1 TACCGGGGTCTCTTCCAGACAGAGAGAGAGGCGGCGCTCTT 50

RESULT 37
US-10-363-345A-30091
; Sequence 30091, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 30091
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-345A-30091

Query Match 3.4%; Score 45; DB 8; Length 837;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 39 TTGAATGAGAGAGAGAGCGCGCGCGCGCGCGCGCGAGGCG 83
|||
Db 418 TTGAATGAGAGAGAGAGCGCGCGCGCGCGCGCGCGAGGCG 462

RESULT 38
US-10-363-345A-30092/C
; Sequence 30092, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 30092
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-345A-30092

Query Match 3.4%; Score 45; DB 8; Length 837;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 39 TTGAATGAGAGAGAGAGCGCGCGCGCGCGCGCGCGAGGCG 83
|||
Db 420 TTGAATGAGAGAGAGAGCGCGCGCGCGCGCGCGCGAGGCG 376

RESULT 39
US-10-363-483A-30091
; Sequence 30091, Application US/103633483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; TITLE OF INVENTION: illnesses
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 30091
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-483A-30091

Query Match 3.4%; Score 45; DB 9; Length 837;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 39 TTGAATGAGAGAGAGAGCGCGCGCGCGCGCGCGCGAGGCG 83
|||
Db 418 TTGAATGAGAGAGAGAGCGCGCGCGCGCGCGCGCGAGGCG 462

RESULT 40
US-10-363-483A-30092/C
; Sequence 30092, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; TITLE OF INVENTION: illnesses
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 30092
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-483A-30092

Query Match 3.4%; Score 45; DB 9; Length 837;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 39 TTGAATGAGAGAGAGAGCGCGCGCGCGCGCGCGCGAGGCG 83
|||
Db 420 TTGAATGAGAGAGAGAGCGCGCGCGCGCGCGCGCGAGGCG 376

RESULT 41
US-09-934-249-12
; Sequence 12, Application US/09934249
; Patent No. US20020115081A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Richard T.
; APPLICANT: Landschulz, Katherine T.
; APPLICANT: Turi, Thomas G.
; APPLICANT: Thompson, John F.
; APPLICANT: Kennedy, Scott P.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
; FILE REFERENCE: P0738/7001/ERP/KA
```


CURRENT APPLICATION NUMBER: US/09/934,249
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 878
TYPE: DNA
ORGANISM: Mus Musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (20)...(841)
US-09-934-249-12

Query Match 3.3%; Score 44; DB 3; Length 878;
Best Local Similarity 100.0%; Pred. No. 4,2e-11;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 875 GGGGAGAGCCCCCACCCTACCAAGGGCCCTGACCTCCAGCT 918
DB 458 GGGGAGAGCCCCCACCCTACCAAGGGCCCTGACCTCCAGCT 501

RESULT 42
US-09-796-753-57
Sequence 57, Application US/09/796,753
Publication No. US20030027998A1
GENERAL INFORMATION:
APPLICANT: McCarthy, Sean A.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-227-999
CURRENT APPLICATION NUMBER: US/09/796,753
PRIOR FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/183,175
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 09/223,094
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/224,246
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/259,388
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/122,458
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: 09/312,359
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/336,536
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 09/342,687
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 09/345,464
PRIOR FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: 09/365,164
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 09/399,723
PRIOR FILING DATE: 1999-09-20
PRIOR APPLICATION NUMBER: 09/409,634
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 09/471,179
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 09/474,071
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/474,072
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/514,010
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: 09/516,745
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/572,002
PRIOR FILING DATE: 2000-05-14
PRIOR APPLICATION NUMBER: 09/597,993

PRIOR FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: 09/599,596
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 09/630,334
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: 09/606,565
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/606,317
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/665,666
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: 09/677,751
PRIOR FILING DATE: 2000-09-30
NUMBER OF SEQ ID NOS: 162
SEQ ID NO 57
LENGTH: 1713
TYPE: DNA
ORGANISM: Mouse
FEATURE:
NAME/KEY: CDS
LOCATION: (2)...(652)
US-09-796-753-57

Query Match 3.3%; Score 44; DB 3; Length 1713;
Best Local Similarity 100.0%; Pred. No. 3,8e-11;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 875 GGGGAGAGCCCCCACCCTACCAAGGGCCCTGACCTCCAGCT 918
DB 269 GGGGAGAGCCCCCACCCTACCAAGGGCCCTGACCTCCAGCT 312

RESULT 43
US-09-934-249-15
Sequence 15, Application US/09/934,249
Patent No. US20020115081A1
GENERAL INFORMATION:
APPLICANT: Lee, Richard T.
APPLICANT: Landeshultz, Katherine T.
APPLICANT: Turt, Thomas G.
APPLICANT: Thompson, John F.
APPLICANT: Kennedy, Scott P.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
FILE REFERENCE: P0738/7001/ERP/KA
CURRENT APPLICATION NUMBER: US/09/934,249
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 15
LENGTH: 475
TYPE: DNA
ORGANISM: Mus Musculus
US-09-934-249-15

Query Match 3.1%; Score 41; DB 3; Length 475;
Best Local Similarity 100.0%; Pred. No. 1,4e-09;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 438 GCACCGCGCGCGCGCGCGCGCGGAGCGCCCATGCTCTGCG 478
DB 33 GCACCGCGCGCGCGCGCGCGCGGAGCGCCCATGCTCTGCG 73

RESULT 44
US-10-363-345A-30089/C
Sequence 30089, Application US/10363345A
Publication No. US20040234960A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock

US-10-425-115-66221

Query Match 2.6%; Score 34; DB 8; Length 555;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 GAGGAGGAGGAGCGCGCGCGCGCGCGCGCGCG 78
DB 387 GAGGAGGAGGAGCGCGCGCGCGCGCGCGCGCG 420

RESULT 49

US-10-856-499-146/c
; Sequence 146, Application US/10856499
; Publication No. US20040259145A1
; GENERAL INFORMATION:
; APPLICANT: Shenk, Michael A.
; APPLICANT: Wood, Marion
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000.1021C2
; CURRENT APPLICATION NUMBER: US/10/856,499
; CURRENT FILING DATE: 2004-05-28
; NUMBER OF SEQ ID NOS: 2370
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 146
; LENGTH: 640
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-856-499-146

Query Match 2.6%; Score 34; DB 8; Length 640;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 GAGGAGGAGGAGCGCGCGCGCGCGCGCGCGCG 78
DB 226 GAGGAGGAGGAGCGCGCGCGCGCGCGCGCGCG 193

RESULT 50

US-10-739-930-3690/c
; Sequence 3690, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovacic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 3690
; LENGTH: 1050
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: GLYMA-23APR03-CLUSTER54078_1
US-10-739-930-3690

Query Match 2.6%; Score 34; DB 8; Length 1050;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 GAGGAGGAGGAGCGCGCGCGCGCGCGCGCGCG 78
DB 422 GAGGAGGAGGAGCGCGCGCGCGCGCGCGCGCG 389

Search completed: February 28, 2006, 11:19:01
Job time: 1213 secs

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C 94	24	1.8	25	8	US-10-310-914A-1065870	Sequence 1065870,	C 167	23	1.7	23	8	US-10-310-914A-1065871	Sequence 1065871,
C 95	24	1.8	27	8	US-10-310-914A-432650	Sequence 432650,	C 168	23	1.7	24	8	US-10-310-914A-78097	Sequence 78097, A
C 96	24	1.8	29	8	US-10-310-914A-707883	Sequence 707883,	C 169	23	1.7	24	8	US-10-310-914A-87752	Sequence 87752,
C 97	24	1.8	520	12	US-11-123-896-373	Sequence 373, App	C 170	23	1.7	24	8	US-10-310-914A-94850	Sequence 94850, A
C 98	24	1.8	637	6	US-09-925-065A-887583	Sequence 887583,	C 171	23	1.7	24	8	US-10-310-914A-94851	Sequence 94851, A
C 99	24	1.8	637	6	US-09-925-065A-911394	Sequence 911394,	C 172	23	1.7	24	8	US-10-310-914A-94852	Sequence 94852, A
C 100	24	1.8	658	6	US-09-925-065A-883427	Sequence 883427,	C 173	23	1.7	24	8	US-10-310-914A-94853	Sequence 94853, A
C 101	24	1.8	836	7	US-09-925-065A-8376	Sequence 8376, Ap	C 174	23	1.7	24	8	US-10-310-914A-122968	Sequence 122968
C 102	24	1.8	855	7	US-10-714-887-127	Sequence 127, App	C 175	23	1.7	24	8	US-10-310-914A-163371	Sequence 163371,
C 103	24	1.8	1719	8	US-10-750-185-24932	Sequence 24932, A	C 176	23	1.7	24	8	US-10-310-914A-163372	Sequence 163372,
C 104	24	1.8	1719	8	US-10-750-623-24932	Sequence 24932, A	C 177	23	1.7	24	8	US-10-310-914A-163373	Sequence 163373,
C 105	24	1.8	5846	12	US-11-136-527-3312	Sequence 3312, Ap	C 178	23	1.7	24	8	US-10-310-914A-167690	Sequence 167690,
C 106	24	1.8	5801	12	US-11-000-463-580	Sequence 580, App	C 179	23	1.7	24	8	US-10-310-914A-167691	Sequence 167691,
C 107	24	1.8	153376	12	US-11-121-086-5	Sequence 5, Appl	C 180	23	1.7	24	8	US-10-310-914A-167692	Sequence 167692,
C 108	24	1.8	162013	12	US-11-150-888-30	Sequence 30, Appl	C 181	23	1.7	24	8	US-10-310-914A-167693	Sequence 167693,
C 109	24	1.8	172543	12	US-11-121-086-6	Sequence 6, Appl	C 182	23	1.7	24	8	US-10-310-914A-167694	Sequence 167694,
C 110	23	1.7	23	8	US-10-310-914A-42427	Sequence 42427, A	C 183	23	1.7	24	8	US-10-310-914A-167695	Sequence 167695,
C 111	23	1.7	23	8	US-10-310-914A-42428	Sequence 42428, A	C 184	23	1.7	24	8	US-10-310-914A-167696	Sequence 167696,
C 112	23	1.7	23	8	US-10-310-914A-42429	Sequence 42429, A	C 185	23	1.7	24	8	US-10-310-914A-167716	Sequence 167716,
C 113	23	1.7	23	8	US-10-310-914A-42430	Sequence 42430, A	C 186	23	1.7	24	8	US-10-310-914A-167717	Sequence 167717,
C 114	23	1.7	23	8	US-10-310-914A-42431	Sequence 42431, A	C 187	23	1.7	24	8	US-10-310-914A-189745	Sequence 189745,
C 115	23	1.7	23	8	US-10-310-914A-42432	Sequence 42432, A	C 188	23	1.7	24	8	US-10-310-914A-189746	Sequence 189746,
C 116	23	1.7	23	8	US-10-310-914A-42433	Sequence 42433, A	C 189	23	1.7	24	8	US-10-310-914A-189747	Sequence 189747,
C 117	23	1.7	23	8	US-10-310-914A-51709	Sequence 51709, A	C 190	23	1.7	24	8	US-10-310-914A-226067	Sequence 226067,
C 118	23	1.7	23	8	US-10-310-914A-78091	Sequence 78091, A	C 191	23	1.7	24	8	US-10-310-914A-226067	Sequence 226067,
C 119	23	1.7	23	8	US-10-310-914A-78092	Sequence 78092, A	C 192	23	1.7	24	8	US-10-310-914A-225937	Sequence 225937,
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C 121	23	1.7	23	8	US-10-310-914A-100311	Sequence 100311,	C 194	23	1.7	24	8	US-10-310-914A-317199	Sequence 317199,
C 122	23	1.7	23	8	US-10-310-914A-100329	Sequence 100329,	C 195	23	1.7	24	8	US-10-310-914A-317200	Sequence 317200,
C 123	23	1.7	23	8	US-10-310-914A-156012	Sequence 156012,	C 196	23	1.7	24	8	US-10-310-914A-317201	Sequence 317201,
C 124	23	1.7	23	8	US-10-310-914A-167370	Sequence 167370,	C 197	23	1.7	24	8	US-10-310-914A-339018	Sequence 339018,
C 125	23	1.7	23	8	US-10-310-914A-167688	Sequence 167688,	C 198	23	1.7	24	8	US-10-310-914A-341341	Sequence 341341,
C 126	23	1.7	23	8	US-10-310-914A-167689	Sequence 167689,	C 199	23	1.7	24	8	US-10-310-914A-341342	Sequence 341342,
C 127	23	1.7	23	8	US-10-310-914A-168050	Sequence 168050,	C 200	23	1.7	24	8	US-10-310-914A-341343	Sequence 341343,
C 128	23	1.7	23	8	US-10-310-914A-168051	Sequence 168051,	C 201	23	1.7	24	8	US-10-310-914A-341344	Sequence 341344,
C 129	23	1.7	23	8	US-10-310-914A-168052	Sequence 168052,	C 202	23	1.7	24	8	US-10-310-914A-368121	Sequence 368121,
C 130	23	1.7	23	8	US-10-310-914A-168053	Sequence 168053,	C 203	23	1.7	24	8	US-10-310-914A-412089	Sequence 412089,
C 131	23	1.7	23	8	US-10-310-914A-168054	Sequence 168054,	C 204	23	1.7	24	8	US-10-310-914A-412090	Sequence 412090,
C 132	23	1.7	23	8	US-10-310-914A-168055	Sequence 168055,	C 205	23	1.7	24	8	US-10-310-914A-412091	Sequence 412091,
C 133	23	1.7	23	8	US-10-310-914A-168056	Sequence 168056,	C 206	23	1.7	24	8	US-10-310-914A-412092	Sequence 412092,
C 134	23	1.7	23	8	US-10-310-914A-168057	Sequence 168057,	C 207	23	1.7	24	8	US-10-310-914A-416117	Sequence 416117,
C 135	23	1.7	23	8	US-10-310-914A-182888	Sequence 182888,	C 208	23	1.7	24	8	US-10-310-914A-430467	Sequence 430467,
C 136	23	1.7	23	8	US-10-310-914A-182893	Sequence 182893,	C 209	23	1.7	24	8	US-10-310-914A-494510	Sequence 494510,
C 137	23	1.7	23	8	US-10-310-914A-182894	Sequence 182894,	C 210	23	1.7	24	8	US-10-310-914A-632071	Sequence 632071,
C 138	23	1.7	23	8	US-10-310-914A-182894	Sequence 182894,	C 211	23	1.7	24	8	US-10-310-914A-691360	Sequence 691360,
C 139	23	1.7	23	8	US-10-310-914A-226060	Sequence 226060,	C 212	23	1.7	24	8	US-10-310-914A-691360	Sequence 691360,
C 140	23	1.7	23	8	US-10-310-914A-226061	Sequence 226061,	C 213	23	1.7	24	8	US-10-310-914A-816478	Sequence 816478,
C 141	23	1.7	23	8	US-10-310-914A-226062	Sequence 226062,	C 214	23	1.7	24	8	US-10-310-914A-844403	Sequence 844403,
C 142	23	1.7	23	8	US-10-310-914A-226063	Sequence 226063,	C 215	23	1.7	24	8	US-10-310-914A-845281	Sequence 845281,
C 143	23	1.7	23	8	US-10-310-914A-226064	Sequence 226064,	C 216	23	1.7	24	8	US-10-310-914A-938142	Sequence 938142,
C 144	23	1.7	23	8	US-10-310-914A-255935	Sequence 255935,	C 217	23	1.7	24	8	US-10-310-914A-983803	Sequence 983803,
C 145	23	1.7	23	8	US-10-310-914A-261088	Sequence 261088,	C 218	23	1.7	24	8	US-10-310-914A-983804	Sequence 983804,
C 146	23	1.7	23	8	US-10-310-914A-346664	Sequence 346664,	C 219	23	1.7	24	8	US-10-310-914A-983805	Sequence 983805,
C 147	23	1.7	23	8	US-10-310-914A-446664	Sequence 446664,	C 220	23	1.7	24	8	US-10-310-914A-1310946	Sequence 1310946,
C 148	23	1.7	23	8	US-10-310-914A-399955	Sequence 399955,	C 221	23	1.7	24	8	US-10-310-914A-1310947	Sequence 1310947,
C 149	23	1.7	23	8	US-10-310-914A-399984	Sequence 399984,	C 222	23	1.7	24	8	US-10-310-914A-1090775	Sequence 1090775,
C 150	23	1.7	23	8	US-10-310-914A-399995	Sequence 399995,	C 223	23	1.7	24	8	US-10-310-914A-1310943	Sequence 1310943,
C 151	23	1.7	23	8	US-10-310-914A-399999	Sequence 399999,	C 224	23	1.7	24	8	US-10-310-914A-1310944	Sequence 1310944,
C 152	23	1.7	23	8	US-10-310-914A-416111	Sequence 416111,	C 225	23	1.7	24	8	US-10-310-914A-1310945	Sequence 1310945,
C 153	23	1.7	23	8	US-10-310-914A-430461	Sequence 430461,	C 226	23	1.7	24	8	US-10-310-914A-1310946	Sequence 1310946,
C 154	23	1.7	23	8	US-10-310-914A-432629	Sequence 432629,	C 227	23	1.7	24	8	US-10-310-914A-1310947	Sequence 1310947,
C 155	23	1.7	23	8	US-10-310-914A-463744	Sequence 463744,	C 228	23	1.7	24	8	US-10-310-914A-1310948	Sequence 1310948,
C 156	23	1.7	23	8	US-10-310-914A-463745	Sequence 463745,	C 229	23	1.7	24	8	US-10-310-914A-1310949	Sequence 1310949,
C 157	23	1.7	23	8	US-10-310-914A-536246	Sequence 536246,	C 230	23	1.7	25	8	US-10-310-914A-51711	Sequence 51711, A
C 158	23	1.7	23	8	US-10-310-914A-536250	Sequence 536250,	C 231	23	1.7	25	8	US-10-310-914A-94854	Sequence 94854, A
C 159	23	1.7	23	8	US-10-310-914A-545337	Sequence 545337,	C 232	23	1.7	25	8	US-10-310-914A-1693350	Sequence 1693350,
C 160	23	1.7	23	8	US-10-310-914A-545438	Sequence 545438,	C 233	23	1.7	25	8	US-10-310-914A-280847	Sequence 280847,
C 161	23	1.7	23	8	US-10-310-914A-576634	Sequence 576634,	C 234	23	1.7	25	8	US-10-310-914A-412093	Sequence 412093,
C 162	23	1.7	23	8	US-10-310-914A-807660	Sequence 807660,	C 235	23	1.7	25	8	US-10-310-914A-633080	Sequence 633080,
C 163	23	1.7	23	8	US-10-310-914A-838215	Sequence 838215,	C 236	23	1.7	25	8	US-10-310-914A-641631	Sequence 641631,
C 164	23	1.7	23	8	US-10-310-914A-875272	Sequence 875272,	C 237	23	1.7	25	8	US-10-310-914A-691353	Sequence 691353,
C 165	23	1.7	23	8	US-10-310-914A-983802	Sequence 983802,	C 238	23	1.7	25	8	US-10-310-914A-691353	Sequence 691353,
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C 249	23	1.7	27	8	US-10-310-914A-1090776	Sequence 1090776,	C 322	23	1.7	3167	6	US-09-925-065A-21764	Sequence 21764, A
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C 310	23	1.7	2400	9	US-11-072-512-228	Sequence 228, App							
C 311	23	1.7	2500	9	US-11-245-147-210	Sequence 210, App							
C 312	23	1.7	2690	9	US-11-072-512-608	Sequence 608, App							

RESULT 1
 US-11-186-284-208
 ; Sequence 208, Application US/11186284
 ; Publication No. US20050266493A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; APPLICANT: Berger, Allison
 ; APPLICANT: Guillemette, Tracy L.
 ; APPLICANT: Kamatkar, Shubhangit
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Monahan, John B.
 ; APPLICANT: Thibodeau, Stephen N.
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
 ; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 ; FILE REFERENCE: MPW01-029P2RNM
 ; CURRENT APPLICATION NUMBER: US/11/186,284
 ; CURRENT FILING DATE: 2005-07-21
 ; PRIOR APPLICATION NUMBER: US/10/301,822
 ; PRIOR FILING DATE: 2002-11-21
 ; PRIOR APPLICATION NUMBER: US 60/339,971
 ; PRIOR FILING DATE: 2001-12-10
 ; PRIOR APPLICATION NUMBER: US 60/361,978
 ; PRIOR FILING DATE: 2002-03-05
 ; PRIOR APPLICATION NUMBER: US 60/381,988
 ; PRIOR FILING DATE: 2002-05-20
 ; NUMBER OF SEQ ID NOS: 228
 ; SOFTWARE: FastSeq for Windows Version 4.0

APPLICANT: Shiler, Kyuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1106
LENGTH: 94
TYPE: RNA
ORGANISM: Human
US-10-310-914A-1106

Query Match 6.0%; Score 79; DB 8; Length 94;
Best Local Similarity 100.0%; Pred. No. 9.3e-30;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1028 TGCCCCCAGAGTAACTCGGCGATCGCCGCAAGTGTCTACGCGAGGGGGGGCGCATG 1087
Db 79 TGCCCCCAGAGTAACTCGGCGATCGCCGCAAGTGTCTACGCGAGGGGGGGCGCATG 20

Qy 1088 GAGGGGGCGCGCCGACCT 1106
Db 19 GAGGGGGCGCGCCGACCT 1

RESULT 5

US-10-310-914A-1107/c
Sequence 1107, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1107
LENGTH: 97
TYPE: RNA
ORGANISM: Human
US-10-310-914A-1107

Query Match 5.5%; Score 72; DB 8; Length 97;
Best Local Similarity 100.0%; Pred. No. 3.3e-26;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1235 TGGAGCAAGAGAGATTAACAGAAAGACCCCTCTAGAGTCCCGAGGGGGCGCGG 1294
Db 72 TGGAGCAAGAGAGATTAACAGAAAGACCCCTCTAGAGTCCCGAGGGGGCGCGG 13

Qy 1295 GCTGGGGCTGCG 1306
Db 12 GCTGGGGCTGCG 1

RESULT 6

US-10-310-914A-7162/c
Sequence 7162, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3
SEQ ID NO 7162
LENGTH: 63
TYPE: RNA
ORGANISM: Human
US-10-310-914A-7162

Query Match 3.9%; Score 51; DB 8; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1130 CCGGGTCTCTCTTCAGACACAGCAGAGCATGCGCCCTCTGCTG 1180
Db 63 CCGGGTCTCTCTTCAGACACAGCAGAGCATGCGCCCTCTGCTG 13

RESULT 7

US-11-072-512-700/c
Sequence 700, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: MAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHICO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOMYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 700
LENGTH: 2332
TYPE: DNA
ORGANISM: Homo sapiens
US-11-072-512-700

Query Match 2.3%; Score 31; DB 9; Length 2332;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 45 GAGGAGAGAGAGAGCGCGCGCGCGCGCGG 75
Db 1225 GAGGAGAGAGAGCGCGCGCGCGCGCGCGG 1195

RESULT 8

US-10-310-914A-399937/c
Sequence 399937, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310.914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 399937
LENGTH: 30
TYPE: RNA
ORGANISM: Human
US-10-310-914A-399937

Query Match 2.2%; Score 29; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1284 AGGGGGCGGGGCTGGGGCTGCGTAGGTG 1312
DB 29 AGGGGGCGGGGCTGGGGCTGCGTAGGTG 1

RESULT 9
US-11-112-944-14
Sequence 14, Application US/11112944
Publication No. US20050244872A1
GENERAL INFORMATION:
APPLICANT: Harris, Cole
TITLE OF INVENTION: Breast Cancer Gene Expression Biomarkers
FILE REFERENCE: 05-325-US
CURRENT APPLICATION NUMBER: US/11/112.944
CURRENT FILING DATE: 2005-04-22
PRIOR APPLICATION NUMBER: US 60/564,757
PRIOR FILING DATE: 2004-04-23
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.3
SEQ ID NO 14
LENGTH: 1546
TYPE: DNA
ORGANISM: Homo sapiens
US-11-112-944-14

Query Match 2.2%; Score 29; DB 10; Length 1546;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 84
DB 439 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 467

RESULT 10
US-11-136-527-144/C
Sequence 144, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136.527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 144
LENGTH: 2947
TYPE: DNA
ORGANISM: Rattus norvegicus
US-11-136-527-144

Query Match 2.2%; Score 29; DB 12; Length 2947;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 GGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 81
DB 85 GGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 57

RESULT 11
US-10-770-726-28/C
Sequence 28, Application US/10770726
Publication No. US20050266409A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
CURRENT APPLICATION NUMBER: US/10/770.726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: PatentIn version 3.2
SEQ ID NO 28
LENGTH: 3131
TYPE: DNA
ORGANISM: Homo sapiens
US-10-770-726-28

Query Match 2.2%; Score 29; DB 8; Length 3131;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 TGAGGAGGAGGAGGCGCGCGCGCGCGCGCGCG 72
DB 227 TGAGGAGGAGGAGGCGCGCGCGCGCGCGCGCG 199

RESULT 12
US-11-121-086-14
Sequence 14, Application US/11121086
Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121.086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.3
SEQ ID NO 14
LENGTH: 167891
TYPE: DNA
ORGANISM: Homo sapiens
US-11-121-086-14

Query Match 2.2%; Score 29; DB 12; Length 167891;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 84
DB 100185 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 100213

RESULT 13
US-10-310-914A-100326
Sequence 100326, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Benitich, Isaac
APPLICANT: Shlifer, Kivuzat

RESULT 17
 US-11-124-367A-4204/c
 Sequence 4204, Application US/11124367A
 Publication No. US20060024700A1
 GENERAL INFORMATION:
 APPLICANT: Michele Cargill
 APPLICANT: Hongjin Huang
 TITLE OF INVENTION: Genetic Polymorphisms Associated with
 TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
 FILE REFERENCE: C1001519.0RD
 CURRENT APPLICATION NUMBER: US/11/124,367A
 CURRENT FILING DATE: 2005-05-09
 PRIOR APPLICATION NUMBER: US 60/568,846
 PRIOR FILING DATE: 2004-05-07
 PRIOR APPLICATION NUMBER: US 60/582,609
 PRIOR FILING DATE: 2004-06-25
 PRIOR APPLICATION NUMBER: US 60/599,554
 PRIOR FILING DATE: 2004-08-09
 NUMBER OF SEQ ID NOS: 34460


```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4204
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-4204
```

```
Query Match      2.1%; Score 28; DB 12; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      51 GAGGAGCGCGCGCGCGCGCGCGCGCGG 78
Db      142 GAGGAGCGCGCGCGCGCGCGCGCGCGG 115
```

```
RESULT 18
US-11-124-367A-4257/c
; Sequence 4257, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: C1001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4257
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-4257
```

```
Query Match      2.1%; Score 28; DB 12; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      51 GAGGAGCGCGCGCGCGCGCGCGCGCGG 78
Db      138 GAGGAGCGCGCGCGCGCGCGCGCGCGG 111
```

```
RESULT 19
US-11-124-367A-4261/c
; Sequence 4261, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: C1001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4261
; LENGTH: 201
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-4261
```

```
Query Match      2.1%; Score 28; DB 12; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      51 GAGGAGCGCGCGCGCGCGCGCGCGCGG 78
Db      96 GAGGAGCGCGCGCGCGCGCGCGCGCGG 69
```

```
RESULT 20
US-11-124-367A-4262/c
; Sequence 4262, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: C1001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4262
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-4262
```

```
Query Match      2.1%; Score 28; DB 12; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      51 GAGGAGCGCGCGCGCGCGCGCGCGCGG 78
Db      40 GAGGAGCGCGCGCGCGCGCGCGCGCGG 13
```

```
RESULT 21
US-11-124-367A-4274/c
; Sequence 4274, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: C1001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4274
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-4274
```


Query Match 2.1%; Score 28; DB 12; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GAGGAGCGCGCGCGCGCGCGCGG 78
DB 142 GAGGAGCGCGCGCGCGCGCGCGG 115

RESULT 22
US-11-124-367A-4325/C
; Sequence 4325, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CLO01519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4325
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-4325

Query Match 2.1%; Score 28; DB 12; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GAGGAGCGCGCGCGCGCGCGCGG 78
DB 138 GAGGAGCGCGCGCGCGCGCGCGG 111

RESULT 23
US-11-124-367A-4329/C
; Sequence 4329, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CLO01519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4329
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-4329

Query Match 2.1%; Score 28; DB 12; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.0007;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GAGGAGCGCGCGCGCGCGCGCGG 78
DB 96 GAGGAGCGCGCGCGCGCGCGCGG 69

RESULT 24
US-11-124-367A-4330/C
; Sequence 4330, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CLO01519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4330
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-4330

Query Match 2.1%; Score 28; DB 12; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GAGGAGCGCGCGCGCGCGCGCGG 78
DB 40 GAGGAGCGCGCGCGCGCGCGCGG 13

RESULT 25
US-11-124-367A-4342/C
; Sequence 4342, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CLO01519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4342
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-4342

Query Match 2.1%; Score 28; DB 12; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GAGGAGCGCGCGCGCGCGCGCGG 78

Db 142 GAGGAGCGCGCGCGCGCGCGCGG 115

RESULT 26
US-11-124-367A-4392/c
; Sequence 4392, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4392
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-4392

Query Match 2.1%; Score 28; DB 12; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 GAGGAGCGCGCGCGCGCGCGCGG 78
Db 138 GAGGAGCGCGCGCGCGCGCGCGG 111

RESULT 27
US-11-124-367A-4396/c
; Sequence 4396, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4396
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-4396

Query Match 2.1%; Score 28; DB 12; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 GAGGAGCGCGCGCGCGCGCGCGG 78
Db 96 GAGGAGCGCGCGCGCGCGCGCGG 69

RESULT 28
US-11-124-367A-4397/c
; Sequence 4397, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4397
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-4397

Query Match 2.1%; Score 28; DB 12; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 GAGGAGCGCGCGCGCGCGCGCGG 78
Db 40 GAGGAGCGCGCGCGCGCGCGCGG 13

RESULT 29
US-11-124-367A-4409/c
; Sequence 4409, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4409
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-4409

Query Match 2.1%; Score 28; DB 12; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 GAGGAGCGCGCGCGCGCGCGCGG 78
Db 142 GAGGAGCGCGCGCGCGCGCGCGG 115

RESULT 30
US-11-124-367A-23494/c


```
Sequence 23494, Application US/11124367A
Publication No. US20060024700A1
GENERAL INFORMATION:
APPLICANT: Michele Cargill
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CL001519.ORD
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR FILING DATE: 2004-08-09
NUMBER OF SEQ ID NOS: 34460
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23494
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-11-124-367A-23494

Query Match
Best Local Similarity 100.0%; Score 28; DB 12; Length 201;
Pred. No. 0.0007;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GAGGAGCGCGCGCGCGCGCGCGCGCGG 78
DB 40 GAGGAGCGCGCGCGCGCGCGCGCGCGG 13

RESULT 31
US-11-124-367A-23495/C
Sequence 23495, Application US/11124367A
Publication No. US20060024700A1
GENERAL INFORMATION:
APPLICANT: Michele Cargill
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CL001519.ORD
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR FILING DATE: 2004-08-09
NUMBER OF SEQ ID NOS: 34460
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23495
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-11-124-367A-23495

Query Match
Best Local Similarity 100.0%; Score 28; DB 12; Length 201;
Pred. No. 0.0007;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GAGGAGCGCGCGCGCGCGCGCGCGCGG 78
DB 96 GAGGAGCGCGCGCGCGCGCGCGCGCGG 69

RESULT 32
US-11-124-367A-23496/C
Sequence 23496, Application US/11124367A
Publication No. US20060024700A1
GENERAL INFORMATION:
```

```
APPLICANT: Michele Cargill
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CL001519.ORD
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US/11/124,367A
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR FILING DATE: 2004-08-09
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR FILING DATE: 2004-08-09
NUMBER OF SEQ ID NOS: 34460
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23496
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-11-124-367A-23496

Query Match
Best Local Similarity 100.0%; Score 28; DB 12; Length 201;
Pred. No. 0.0007;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GAGGAGCGCGCGCGCGCGCGCGCGCGG 78
DB 138 GAGGAGCGCGCGCGCGCGCGCGCGCGG 111

RESULT 33
US-11-124-367A-23708/C
Sequence 23708, Application US/11124367A
Publication No. US20060024700A1
GENERAL INFORMATION:
APPLICANT: Michele Cargill
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CL001519.ORD
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US/11/124,367A
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR FILING DATE: 2004-08-09
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR FILING DATE: 2004-08-09
NUMBER OF SEQ ID NOS: 34460
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23708
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-11-124-367A-23708

Query Match
Best Local Similarity 100.0%; Score 28; DB 12; Length 201;
Pred. No. 0.0007;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GAGGAGCGCGCGCGCGCGCGCGCGCGG 78
DB 142 GAGGAGCGCGCGCGCGCGCGCGCGCGG 115

RESULT 34
US-11-024-959-254/C
Sequence 254, Application US/11024955
Publication No. US20060010516A1
GENERAL INFORMATION:
APPLICANT: FORSTER, RICHARD L.
APPLICANT: CONNETT, MARIE B.
APPLICANT: EMERSON, SARAH JANE
```


? APPLICANT: GRIGOR, MURRAY ROBERT
 ? APPLICANT: HIGGINS, COLLEEN M.
 ? APPLICANT: LUND, STEVEN TROY
 ? APPLICANT: MAGNUSIN, ANDREAS
 ? APPLICANT: KODRZYCKI, BOB
 ? TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
 ? FILE REFERENCE: 044463-0360
 ? CURRENT APPLICATION NUMBER: US/11/024,959
 ? CURRENT FILING DATE: 2004-12-30
 ? PRIOR APPLICATION NUMBER: 60/533,036
 ? PRIOR FILING DATE: 2003-12-30
 ? NUMBER OF SEQ ID NOS: 782
 ? SOFTWARE: PatentIn version 3.3
 ? SEQ ID NO 254
 ? LENGTH: 2097
 ? TYPE: DNA
 ? ORGANISM: *Bucalalyptus* sp.
 ? US-11-024-959-254

Query Match	2.1%	Score 28:	DB 12;	Length 2097;
Best Local Similarity	100.0%;	Pred. No.	0.00066;	
Matches 28;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Oy 56 GCGGCGGCGGCGGCGGCGGCGGAAGCG 83
 |||||
Db 214 GCGGCGGCGGCGGCGGCGGCGGAGCG 187

```

RESULT 35
US-11-136-527-3064
; Sequence 3064, Application US/1136527
; Publication No. US2005028750A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-04100 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3064
LENGTH: 5453
TYPE: DNA
ORGANISM: Rattus norvegicus
US-11-136-527-3064

```

Query Match	2.1%	Score 28	DB 12	Length 5453
Best Local Similarity	100.0%	Pred. NO.	0.00064	
Matches 28, Conservative	0	Mismatches	0	Gaps 0

[illegible]

```

RESULT 36
US-11-124-367A-206/c
; Sequence 206, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.0BD
; CURRENT APPLICATION NUMBER: US/11/124.367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609

```

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? PRIOR FILING DATE: 2004-06-25
? PRIOR APPLICATION NUMBER: US 60/599,555
? PRIOR FILING DATE: 2004-08-09
? NUMBER OF SEQ ID NOS: 34460
? SOFTWARE: FRETSEQ for Windows Version 4
? SEQ ID NO: 206
? LENGTH: 12200
? TYPE: DNA
? ORGANISM: Homo Sapiens
? US-11-124-367A-206

```

Query Match	2.1 %	Score 28	DB 12	Length 12300
Best Local Similarity	Pred. No. 0.00062			
Matches 28	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy 51 GAGGAGCGGCGGCGGCGGCGGCGGCGG 78
462 GAGGAGCGGCGGCGGCGGCGGCGGCGGCGG 435
Db

```

RESULT 37
US-11-124-367A-207/c
; Sequence 207, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124.367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 12728
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-124-367A-207

```

Query Match	2.1%	Score 28	DB 12	length 12728
Best Local Similarity	100.0%	Pred. No.	0.00062	
Matches 28	Conservative 0	Mismatches 0	Indels 0	Gaps 0

[illegible]

RESULT 38
US-11-124-367A-204/C
: Sequence 204, Application US/11124367A
: Publication No. US20060024700A1
: GENERAL INFORMATION:
: APPLICANT: Michele Cargill
: APPLICANT: Hongjin Huang
: TITLE OF INVENTION: Genetic Polymorphisms Associated with
: TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
: FILE REFERENCE: CI001519.ORD
: CURRENT APPLICATION NUMBER: US/11/124.367A
: CURRENT FILING DATE: 2005-05-09
: PRIOR APPLICATION NUMBER: US 60/568,846
: PRIOR FILING DATE: 2004-05-07
: PRIOR APPLICATION NUMBER: US 60/582,609
: PRIOR FILING DATE: 2004-06-25
: PRIOR APPLICATION NUMBER: US 60/599,554
: PRIOR FILING DATE: 2004-08-09

NUMBER OF SEQ ID NOS: 34460
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 204
LENGTH: 13643
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-124-367A-204

Query Match 2.1%; Score 28; DB 12; Length 13643;
Best Local Similarity 100.0%; Pred. No. 0.00062;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GAGAGGCGCGCGCGCGCGCGCGCGCG 78
DB 462 GAGAGGCGCGCGCGCGCGCGCGCGCG 435

RESULT 39
US-11-124-367A-205/C

Sequence 205, Application US/11124367A
Publication No. US20060024700A1
GENERAL INFORMATION:
APPLICANT: Michele Cargill
APPLICANT: Hongjin Huang
TITLE OF INVENTION: Genetic Polymorphisms Associated with
FILE REFERENCE: CLO01519.ORD
CURRENT APPLICATION NUMBER: US/11/124,367A
PRIOR FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR FILING DATE: 2004-08-09
NUMBER OF SEQ ID NOS: 34460
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 205
LENGTH: 13653
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-124-367A-205

Query Match 2.1%; Score 28; DB 12; Length 13653;
Best Local Similarity 100.0%; Pred. No. 0.00062;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GAGAGGCGCGCGCGCGCGCGCGCGCG 78
DB 462 GAGAGGCGCGCGCGCGCGCGCGCGCG 435

RESULT 40
US-11-055-035-2/C

Sequence 2, Application US/11055035
Publication No. US20050256072A1
GENERAL INFORMATION:
APPLICANT: ARONIN, NEIL
APPLICANT: ZAMORE, PHILIP D.
APPLICANT: BRODERICK, JENNIFER
TITLE OF INVENTION: DUAL FUNCTIONAL OLIGONUCLEOTIDES FOR USE IN REPRESSING
FILE REFERENCE: UMY-095
CURRENT APPLICATION NUMBER: US/11/055,035
PRIOR FILING DATE: 2005-02-09
PRIOR APPLICATION NUMBER: 60/543,467
PRIOR FILING DATE: 2004-02-09
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO: 2
LENGTH: 13672
TYPE: DNA
ORGANISM: Homo sapiens

US-11-055-035-2

Query Match 2.1%; Score 28; DB 12; Length 13672;
Best Local Similarity 100.0%; Pred. No. 0.00062;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GAGAGGCGCGCGCGCGCGCGCGCGCG 78
DB 469 GAGAGGCGCGCGCGCGCGCGCGCGCG 442

RESULT 41
US-10-310-914A-4814

Sequence 4814, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiller, Kyuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
PRIOR FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 4814
LENGTH: 110
TYPE: RNA
ORGANISM: Human
US-10-310-914A-4814

Query Match 2.0%; Score 27; DB 8; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 AGAGAGGCGCGCGCGCGCGCGCGCGCG 75
DB 79 AGAGAGGCGCGCGCGCGCGCGCGCGCG 105

RESULT 42
US-10-310-914A-12973

Sequence 12973, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiller, Kyuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
PRIOR FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 12973
LENGTH: 110
TYPE: RNA
ORGANISM: Human
US-10-310-914A-12973

Query Match 2.0%; Score 27; DB 8; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 AGAGAGGCGCGCGCGCGCGCGCGCGCG 75
DB 79 AGAGAGGCGCGCGCGCGCGCGCGCGCG 105

RESULT 43

US-10-310-914A-20511
Sequence 20511, Application US/10310914A
Publication No. US20060003322A1


```

; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20511
; LENGTH: 110
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-20511

Query Match          2.0%; Score 27; DB 8; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 49 AGAGAGCGCGCGCGCGCGCGCGCGCG 75
Db 79 AGGAGAGCGCGCGCGCGCGCGCGCGCG 105

RESULT 44
US-09-925-065A-373740/c
; Sequence 373740, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 373740
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-373740

Query Match          2.0%; Score 27; DB 6; Length 552;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 GCGCGCGCGCGCGCGCGCGCGCGAGGC 82
Db 305 GCGCGCGCGCGCGCGCGCGCGCGAGGC 279

RESULT 45
US-09-925-065A-540849
; Sequence 540849, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
```

```

; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 540849
; LENGTH: 583
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-540849

Query Match          2.0%; Score 27; DB 6; Length 583;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 AGAGAGCGCGCGCGCGCGCGCGCGCG 78
Db 412 AGGAGCGCGCGCGCGCGCGCGCGCGG 438

RESULT 46
US-09-925-065A-540850
; Sequence 540850, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 540850
; LENGTH: 583
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-540850

Query Match          2.0%; Score 27; DB 6; Length 583;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 AGAGAGCGCGCGCGCGCGCGCGCGCG 78
Db 412 AGGAGCGCGCGCGCGCGCGCGCGCGG 438

RESULT 47
US-09-925-065A-499554/c
; Sequence 499554, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
```


TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925, 065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 499554
LENGTH: 665
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-499554

Query Match 2.0%; Score 26; DB 6; Length 665;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 GGCGCGCGCGCGCGCGCGCGGAG 81
DB 189 GGCGCGCGCGCGCGCGCGCGGAG 164

RESULT 48
US-11-136-527-2759
Sequence 2759, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2759
LENGTH: 1598
TYPE: DNA
ORGANISM: Rattus norvegicus
US-11-136-527-2759

Query Match 2.0%; Score 26; DB 12; Length 1598;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 GGAGGAGCGCGCGCGCGCGCGG 75
DB 499 GGAGGAGCGCGCGCGCGCGCGG 524

RESULT 49
US-11-136-527-2522
Sequence 2522, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294

PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2522
LENGTH: 2074
TYPE: DNA
ORGANISM: Rattus norvegicus
US-11-136-527-2522

Query Match 2.0%; Score 26; DB 12; Length 2074;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 GGAGCGCGCGCGCGCGCGCGGCG 78
DB 262 GGAGCGCGCGCGCGCGCGCGGCG 287

RESULT 50
US-10-750-185-34757
Sequence 34757, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 34757
LENGTH: 2127
TYPE: DNA
ORGANISM: Bovine 1986688111285
US-10-750-185-34757

Query Match 2.0%; Score 26; DB 8; Length 2127;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 GGAGCGCGCGCGCGCGCGCGGCG 78
DB 1117 GGAGCGCGCGCGCGCGCGCGGCG 1142

Search completed: February 28, 2006, 11:27:00
Job time : 485 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2006, 08:31:33 ; Search time 7076.01 Seconds
(without alignments)
10611.945 Million cell updates/sec

Title: US-09-934-249-1

Perfect score: 1321
Sequence: 1 cgaccgcggtctcgagcaga.....ctgcgtagctgaaagcag 1321

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 5683141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

GenEmbl:
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_ov:*
5: gb_ov:*
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14: gb_hlg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1321	100.0	1321	6	AX392417 Sequence
2	1302	93.0	4930	6	CS130796 Sequence
3	1229	93.0	4839	6	CQ812357 Sequence
4	1229	93.0	4839	6	CQ896247 Sequence
5	1229	93.0	4839	6	CQ976475 Sequence
6	1229	93.0	4839	6	CQ981430 Sequence
7	1229	93.0	4839	6	AF305616 Sequence
8	1227.4	92.9	1383	6	AX775889 Sequence
9	909	68.8	4519	6	CQ894692 Sequence
10	887.4	67.2	1061	8	BC015918 Homo sapi
11	861	65.2	861	6	AX392419 Sequence
12	803.2	60.8	969	6	BD272494 Secretd
13	802.2	60.7	1141	8	AF224278 Homo sapi
14	801.8	60.7	4538	6	CS130841 Sequence
15	801.6	60.7	1913	6	BD272544 Secretd
16	801.6	60.7	969	6	BD272514 Secretd
17	801.6	60.7	969	6	BD272515 Secretd
18	801.6	60.7	969	6	BD272516 Secretd

19	801.6	60.7	1140	6	AR336830 Sequence
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21	800	60.6	1818	8	AY128643 Homo sapi
22	800	60.6	4531	6	CS130842 Sequence
23	797.4	60.4	1060	8	BC080635 Homo sapi
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25	755.4	57.2	759	6	BD272545 Secretd
26	751.2	56.9	756	6	BD272495 Secretd
27	750.4	56.8	753	6	BD272513 Secretd
28	630	47.7	1379	9	BC036995 Mus muscu
29	618.6	46.8	1079	9	BC023092 Mus muscu
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31	614.6	46.5	878	9	BC092094 Mus muscu
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34	594.4	45.0	130435	8	HS178077 Homo sapi
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37	565.6	42.8	1265	5	AJ720618 Gallus ga
38	522.8	39.6	150224	8	HS105917 Human DNA
39	493.6	37.4	1693	6	AX392430 Sequence
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43	464.6	35.2	1713	6	BD272517 Secretd
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ALIGNMENTS

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LOCUS	AX392417	Sequence 1 from Patent WO0216416.			
DEFINITION	AX392417				
ACCESSION	AX392417.1	GI:19700732			
VERSION	AX392417.1	GI:19700732			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE	Lee,R.T., Landschulz,K.T., Kennedy,S.P., Thompson,J.F. and Turi,T.G.				
AUTHORS					
TITLE	Diagnosis and treatment of cardiovascular conditions				
JOURNAL	Patent: WO 0216416-A.1 28-FEB-2002;				
FEATURES	THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; PFIZER INC. (US)				
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	/protein_id="CAD29005.1"				
	/db_xref="GI:19700732"				
	/translation="MHRIMGVNSTRFAAAGQPNVSCNCKRSLFQSMETLEFVOI IIVVMMVAVITCLSHYKLSRSTISHSGQRREDLSSGCIWPSRSTVSGN GIPEQVYAPRPDRLAVPPFAQERFHRTPYVQSHIDLPFTISLSDGSRPP YQGPCTOLRDEQOLETRNSVAPRRTIFSDLDMSATRLGCPSPSSGTSATC YSGGRMGPEPTSEVIGHYFGSSFFHQSSGPPSLGLETRLHTHTIAPLESAAIWS KEKQKQKHPL"				
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Query Match	100.0%; Score 1321; DB 6; Length 1321;				
Best Local Similarity	100.0%; Pred. No. 5.3e-142;				
Matches 1321; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 CGACCGCGGTCTCGAGCAAAACCGAGTCTCTTGACTTAATGAGAGGAGGCGG 60				

1 CGACCGCGCTCTCGGAGGAAACCGAATCTCTTGAGATTGAGAGAGAGAGGCG 60
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61 CGCGCGCGCGCGCGCGCGCGCTCGCTGAGGAAAGCTAGCGGAGAGGCTAGCC 120
121 GCGCGGAGCGCGCGCGCGCGCTGAGGAAAGCTAGCGGAGAGGCTAGCC 180
121 GCGCGGAGCGCGCGCGCGCGCTGAGGAAAGCTAGCGGAGAGGCTAGCC 180
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361 CGCGCGCGCGCGCGCGCGCGCGCTGAGGAAAGCTAGCGGAGAGGCTAGCC 420
361 CGCGCGCGCGCGCGCGCGCGCGCTGAGGAAAGCTAGCGGAGAGGCTAGCC 420
421 CTGATGAGGAGGCTCAACAGCAGCGCGCGCGCGCTGAGGAAAGCTAGCGG 480
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601 CCACACTACAGAGCTGTGTCAGCGCTCTTATATACCGCGGACAGCGGCGGAGAGA 660
661 AGATGCGCGCTCTCTGAGAGAGATGCTGTCGCGCTCTGAGAGAGAGAGTCA 720
661 AGATGCGCGCTCTCTGAGAGAGATGCTGTCGCGCTCTGAGAGAGAGAGTCA 720
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901 GATGAGCTGTGTCAGCGCTCTTATATACCGCGGACAGCGGCGGAGAGA 960
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1261 AGGACACCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1320
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1321 G 1321
1321 G 1321

RESULT 2
CS130796
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1
ORRHOFF, T. F.
AUTHORS
TITLE
JOURNAL
Aros Applied Biotechnology APS (DX)
FEATURES
source
1..4930
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="transmembrane, prostate androgen induced RNA (T")

ORIGIN
Query Match 98.6%; Score 1302; DB 6; Length 4930;
Best Local Similarity 100.0%; Pred. No. 5; Se-140; Indels 0; Gaps 0;
Matches 1302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 AACCCGATCTCTTGGACTTGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
80 GGCCTCTGAGGAG 139
61 GGCCTCTGAGGAG 120
140 CTGCAAGCCATTTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 199
121 CTGCAAGCCATTTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
200 GGGAGAGCGGGAG 259
181 GGGAGAGCGGGAG 240
260 GGAACCTTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 319
241 GGAACCTTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
320 CTGATGAGGAG 379
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380 CCGCGCGCGCGCGCGCGCGCGCGCTGAGGAAAGCTAGCGGAGAGGCTAGCC 439

QY 873 ACCGGGAGAGAGCCCGCAACCTTACCAAGGACCCCTGCACTTCCAGACTTCCGGACCCCGAGC 932
Db 781 ACCGGGAGAGAGCCCGCAACCTTACCAAGGACCCCTGCACTTCCAGACTTCCGGACCCCGAGC 840
QY 933 AGCAGCTGGAAGTGAACCCGGAGTCCGTCGCGACGCCCAAGAAAGAAACATCTTTCACA 992
Db 841 AGCAGCTGGAAGTGAACCCGGAGTCCGTCGCGACGCCCAAGAAAGAAACATCTTTCACA 900
QY 993 GTGACCTGATGATAGTGCACAGGCTGCGGAGCCCTGCGCCCGCCAGCAAGTAACTCGGACA 1052
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QY 1053 TCACAGCGCACTGCTGACGCGACGCGCGGCGCAATGAGAGGGCGCCCGCCCACTTACAGCG 1112
Db 961 TCACAGCGCACTGCTGACGCGACGCGCGGCGCAATGAGAGGGCGCCCGCCCACTTACAGCG 1020
QY 1113 AGGTCAATCGGCACTAACCCGGGAGTCTCTCTTCCAGACACAGACAGAGAGAGTGGCGGCT 1172
Db 1021 AGGTCAATCGGCACTAACCCGGGAGTCTCTCTTCCAGACACAGACAGAGAGAGTGGCGGCT 1080
QY 1173 CTTTGTGAGAGGAGACCCGCGTCCACACACACATCGCGCCCTTACAGAGCGCAGCCA 1232
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QY 1293 GGGCTGGGGCTGCGTAGGTGAAAAAGGCAG 1321
Db 1201 GGGCTGGGGCTGCGTAGGTGAAAAAGGCAG 1229

RESULT 4
LOCUS CO896247 4839 bp DNA linear PAT 05-NOV-2004
DEFINITION Sequence 71 from Patent WO2004076614.
ACCESSION CO896247
VERSION CO896247.1 GI:55468096
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
AUTHORS Hitzmann, B., Dahl, E., Rosenthal, A., Specht, T., Schmitt, A.,
Beckmann, G., Bruemendorf, T., Kinemann, H., Roepcke, S., Hermann, K.,
Xinzhong, J., Pilarsky, C. and Staud, B.
TITLE Human nucleic acid sequences obtained from prostatic carcinomas
JOURNAL Patent: WO 2004076614-A 71 10-SEP-2004;
Hitzmann, Bernd (DE); Dahl, Edgar (DE); Rosenthal, Andre (DE);
Specht, Thomas (DE); Schmitt, Armin (DE)
FEATURES
source 1. 4839
/organism="Homo sapiens"
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ORIGIN
Query Match 93.0%; Score 1229; DB 6; Length 4839;
Best Local Similarity 100.0%; Pred. No. 1,2e-11;
Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 GAAAGCTAGAGCGGAGAGCTCAGCCCGGCGGAGCGCGCGCCCGTGCAGCCCAATT 152
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QY 153 TTCCGAGCGCAACCCGCGGCGCACTGCGACGCGCCCGGCGGCTGCCGAGAGCGCGGG 212
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QY 213 GGGCGAGCGGAGCGGAGTCCCGCGCACTGAGCCCGCGGCGCCCGGGAATTTGGCGGC 272
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QY 453 CCGCGGCGAGCCCAATGTCTCTGCAAGTGCACCTGCAACGCTTTGTTCCAGAGCA 512
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QY 873 ACCGGGAGAGAGCCCGCAACCTTACAGAGCCCGCTTCCAGAGTTCGAGACCCCGAGC 932
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Db 1201 GGGCTGGGGCTGCTGAGTGAAGGCGAG 1229

RESULT 5
LOCUS CQ976475 4839 bp DNA linear PAT 19-JAN-2005
DEFINITION Sequence 166 from Patent WO2004113571.
ACCESSION CQ976475
VERSION CQ976475.1 GI:57975803
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS Einstein, R., McGowan, K.M. and Pando, M.P.
TITLE Prostate specific genes and the use thereof as targets for prostate
JOURNAL Cancer therapy and diagnosis
Patent: WO 2004113571-A 166 29-DEC-2004;
Exonhit Therapeutics S.A. (FR)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 93.0%; Score 1229; DB 6; Length 4839;
Best Local Similarity 100.0%; Fred. No. 1.2e-131;
Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGAAGCTAGCGGAGAGGCTCAGCCCGCGGCGAGCGCGCGCGCTGCGAGCCCAAT 60
Qy 153 TTCCGAGCGGAGCGGCGGCGGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 212
Db 61 TTCCGAGCGGAGCGGCGGCGGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
Qy 213 GGGCGGAGGAGCGCGGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 272
Db 121 GGGCGGAGGAGCGCGGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Qy 273 GACCGAGCGCGGAGCGGCGGCGGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 332
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Qy 333 CCGAGCTCGGAGCGGCGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 392
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DEFINITION Sequence 285 from Patent EP1498424.
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VERSION CQ981430.1 GI:58190720
KEYWORDS

SOURCE Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS Rosenthal, A., Hermann, K., Heiden, E., Pilarsky, C., Bruemendorf, T.,
Staub, E., Roepcke, S., Memerich, D., Kinneemann, H. and Li, X.
TITLE Human nucleic acid sequences from lung tumours
JOURNAL Patent: EP 1498424-A 285 19-JAN-2005;
Hinzmann, Bernd (DE); Hermann, Klaus (DE); Heiden, Esmeralda (DE);
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DEFINITION				
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VERSION				
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Homidae; Homo.				
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KEYWORDS			
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Dd	61 ACGCTCTTTGTTCCAGACATGAGATACAGGAGCTGGAGTTTGTTCAGATCATCATCAT 120		
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Dd	121 CCGTGAGTGATGATGTGATGTGTGTGTATCATCGTCTGCTGAGCCACTAACAGT 180		
OY	613 GTCTGCAAGGTCTTCATCAAGCCGGGACAAGCGAGGGGGAGAGAAGAAGATGCCCTGTC 672		
Dd	181 GTCTGCAAGGTCTTCATCAAGCCGGGACAAGCGAGGGGGAGAGAAGAAGATGCCCTGTC 240		
OY	673 CTCAAGAGATGCGTGTGAGCCCTCGGAGAGACAATGTCAAGGCAACGNAATCCAGAGCC 732		
Dd	241 CTCAAGAGATGCGTGTGAGCCCTCGGAGAGACAATGTCAAGGCAACGNAATCCAGAGCC 300		
OY	733 GCAGGTCTACGCCCCGCTCGAGCCACCGACCGCTGCGCCGTGCGCCCTTGCCCAAGC 792		
Dd	301 GCAGGTCTACGCCCCGCTCGAGCCACCGACCGCTGCGCCGTGCGCCCTTGCCCAAGC 360		
OY	793 GGAGGCTTTCACCGCTTTCAGGCCCACTATTCGTAACCTGAGACAGAGATGACCTGCG 852		
Dd	361 GGAGGCTTTCACCGCTTTCAGGCCCACTATTCGTAACCTGAGACAGAGATGACCTGCG 420		
OY	853 ACCGACCATTCGTGTGAGAGAGGGGAGAGAGGCCCCCACTTACAGGAGCCCTCTGACCT 912		

Db	421	GCCTCATTCTTGCTGTACAGCGGGGAGAGCCCTCCATCCAGGGCCCTTGCACCTT	480
Qy	913	CCAGCTTCGGGACCCCGACGACAGCTGGAACTGAAACCGGAGTGGTGGCGCACCC	972
Db	481	CCAGCTTCGGGACCCCGACGACAGCTGGAACTGAAACCGGAGTGGTGGCGCACCC	540
Qy	973	AAACGAAACCATCTTTCGACAGTGACCTGATGATATGTGCGAGCTGGCGGCTCTGCC	1033
Db	541	AAACGAAACCATCTTTCGACAGTGACCTGATGATATGTGCGAGCTGGCGGCTCTGCC	600
Qy	1033	CCCCAGCAGTAACCTCGGGCATCAGGGCCACGTGTCACGGCAGCGGGCGGGCGCATGAGGG	1092
Db	601	CCCCAGCAGTAACCTCGGGCATCAGGGCCACGTGTCACGGCAGCGGGCGGGCGCATGAGGG	660
Qy	1093	GGCGCGGCGCCACTTCACGAGAGTCATCGGCGCACTACCGCGGGGCTCTCTTCACGACCA	1152
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Qy	1153	GCAGAGCAGTGGGCGGCCCTCTCTTGGCTGGAGGGGAGCCGGCTCCACACACACATCGC	1212
Db	721	GCAGAGCAGTGGGCGGCCCTCTCTTGGAGGGGAGCCGGCTCCACACACACATCGC	780
Qy	1213	GGCCCTTAAGAGCGCAGCCATCTTGAAGCAAGAGAAAGATTAACAGAAAGCACCTCTT	1272
Db	781	GGCCCTTAAGAGCGCAGCCATCTTGAAGCAAGAGATTAACAGAAAGCACCTCTT	840
Qy	1273	CTAGGGTCCCCAGGGGGGCGGGGCTGGGGCTGAGGAGAAAGAGCAAG	1321
Db	841	CTAGGGTCCCCAGGGGGGCGGGGCTGAGGAGTGAAGAAAGAGCAAG	889

RESULT 11	AX392419	861 bp	DNA	linear	PAT 23-MAR-2002
LOCUS	AX392419				
DEFINITION	Sequence 3 from Patent WO0216416.				
ACCESSION	AX392419				
VERSION	AX392419.1	GI:19700734			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
	Homnidae; Homo.				
REFERENCE	1				
AUTHORS	Lee, R. T., Landschulz, K. T., Kennedy, S. P., Thompson, J. F. and				
	Tsui, T. G.				
TITLE	Diagnostics and treatment of cardiovascular conditions				
JOURNAL	Patent: WO 0216416-A 3 28-FEB-2002;				
	THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; PFIZER INC. (US)				
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	Best Local Similarity	100.0%;	Pred. No. 2,1e-89;		
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RESULT 12	
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LOCUS	BD272494 969 bp DNA linear
DEFINITION	Secreted proteins and nucleic acids encoding them.
ACCESSION	BD272494
VERSION	BD272494.1 GI:33082262
KEYWORDS	JF 2002539773-A/3.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Cranita; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 969)

AUTHORS Barnes, T.M., Holtzman, D.A., Sharp, J.D. and Fraser, C.C.
TITLE Secreted proteins and nucleic acids encoding them
JOURNAL Patent: JP 2002539773-A 3 26-NOV-2002;
 MILLENNIUM PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
 PN JP 2002539773-A/3

PD 26-NOV-2002
 PF 01-MAR-2000 JP 2000602247
 PR 01-MAR-1999 US 60/122458
 PI THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CHRISTOPHER C FRASER
 PC C12N15/09, C07K14/47, C07K16/18, C12N5/10, C12P21/02, C12Q1/68, PC
 GO1N33/15, GO1N33/50, GO1N33/53, GO1N33/56, C12N15/00, C12N5/00 CC
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Location/Qualifiers
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 Best Local Similarity 99.6%; Pred. No. 8e-83; Indels 0; Gaps 0;
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 62 GGTGTGTGTGATCAGTGTGCTGTCTAGGCACTACAAAGCTGTCTGACGCTCTCATG 121
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 Oy 1294 GGTGAG 1321
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RESULT 13
LOCUS AF224278 1141 bp mRNA linear PRI 18-JUL-2000
DEFINITION Homo sapiens PMEPAL protein (PMEPAL) mRNA, complete cds.
ACCESSION AF224278
VERSION AF224278.1 GI:9255808
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.

REFERENCE
AUTHORS Xu, L.L., Shanmugam, N., Segawa, T., Sesterhenn, I.A., McLeod, D.G.,
 Moul, J.W. and Srivastava, S.
TITLE A novel androgen-regulated gene, PMEPAL, located on chromosome
 20q13 exhibits high level expression in prostate
JOURNAL Genomics 66 (3), 257-263 (2000)
PUBMED 10873380
REFERENCE 2 (bases 1 to 1141)
 Xu, L.L., Shanmugam, N., Segawa, T., Sesterhenn, I.A., McLeod, D.G.,
 Moul, J.W. and Srivastava, S.
AUTHORS Direct Submission
 Submitted (12-JAN-2000) CPDR, USUHS, 1530 East Jefferson Street,
 Rockville, MD 20852, USA

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ORIGIN

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 Db 77 TCTCCTGAGAAACAGGCAATGGCGAGCTGAGTTGTTGATCATCATCATGTTGTT 136

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Dp	137	GGTATGATGGTGAATGGTGGTGGTGAATACAGCGCTCTGTGAGCCACTCAAGCTGTGCG	196
OY	619	ACGGTCTTTCATCAGCCCGGCAACAGCCAGGGGGCGAGAGAGAGATGCTGTCTCTCAGA	678
Dp	197	ACGGTCTTTCATCAGCCCGGCAACAGCCAGGGGGCGAGAGAGATGCTGTCTCTCAGA	256
OY	679	AGGATGCTGTGGCCCTCTGGAGAGACAAGTGTCAAGGCAACGAAATCCAGAGCCGCAAGT	738
Dp	257	AGGATGCTGTGGCCCTCTGGAGAGACAAGTGTCAAGGCAACGAAATCCAGAGCCGCAAGT	316
OY	739	CTAAGCCCGGCGCTGGGCGCCACCGAACGGCGTGGCCGTGCGCCCTTCCGCCAGCGGAGCG	798
Dp	317	CTAAGCCCGGCGCTGGGCGCCACCGAACGGCGTGGCCGTGCGCCCTTCCGCCAGCGGAGCG	376
OY	799	CTTCCACCGCTTCCAGCCCACTTATCCGTAACCTTGACGACGAGATGCACTTGCCACCCAG	858
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OY	859	CATCTCGCTGTCAAGCCGGGAGAGAGCCCCCACCCTTACAGAGGCCCTTGACCTTCAAGCT	918
Dp	437	CATCTCGCTGTCAAGCCGGGAGAGAGCCCCCACCCTTACAGAGGCCCTTGACCTTCAAGCT	496
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Dp	497	TGGGAGCCCCGAGCGAGCACTGGAACTGAACCGGGAGTCCGTTGCGCGGACCCCCAAAG	556
OY	979	AACCATCTTCGACAGTGAACCTGATGGATAGTGCCAGGCTGGGCGGCCCCCTGCCCGAG	1038
Dp	557	AACCATCTTCGACAGTGAACCTGATGGATAGTGCCAGGCTGGGCGGCCCCCTGCCCGAG	616
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Dp	737	CAGTGGGCGCGCCTCTTGTCTGGAGGGGAACCCGAGCTCCACACACACATCGCGCCCT	796
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LOCUS	CS130841	4538 bp	DNA	linear	PAT 02-AUG-2005
DEFINITION	Sequence 127 from Patent WO2005064009.				
ACCESSION	CS130841				
VERSION	CS130841.1	GI:71792911			
KEYWORDS					
SOURCE	.				
ORGANISM	Homo sapiens (human)				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1				
AUTHORS	Oernicott, T.F.				
TITLE	Classification of cancer				
JOURNAL	Patent: WO 2005064009-A 127 14-JUN-2005;				
	Aros Applied Biotechnology APS (DK)				
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Best Local Similarity	-98.4%;	Pred. No. 6.8e-83;		
Matches 810;	Conservative 0;	Mismatches 13;	Indels 0;	Gaps 0;

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BD272544	
ACCESSION	BD272544.1 GI:33082312
VERSION	

KEYWORDS JP 2002539773-A/53.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 1913)
 AUTHORS Barnes,T.M., Holtzman,D.A., Sharp,J.D. and Fraser,C.C.
 TITLE Secreted proteins and nucleic acids encoding them
 JOURNAL Patent: JP 2002539773-A 53 26-NOV-2002;
 MILLENNIUM PHARMACEUTICALS INC
 COMMENT OS Homo sapiens (human)
 PN JP 2002539773-A/53
 PD 26-NOV-2002
 PF 01-MAR-2000 JP 2000602247
 PR 01-MAR-1999 US 60/122458
 PI THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CHRISTOPHER C
 PI FRASER
 PC C12N15/09, C07K14/47, C07K16/18, C12N5/10, C12P21/02, C12Q1/68, PC
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 PC GOIN33/50, GOIN33/53, GOIN33/53, GOIN33/566, C12N15/00, C12N5/00 CC
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 Best Local Similarity 98.3%; Pred. No. 9,6e-83;
 Matches 809; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
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 DB 127 TCTCTCGGAAACCGAGCATGCGAGCTGAGTTTGTTCAGATCATCATCATGTGTGT 186
 QY 559 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 618
 DB 187 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 246
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 DB 247 ACGTCTTTCATCAGCCGCGCACAGCGGCGGAGAGAGAGAGATGCCCTGTCTCAGA 306
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 DB 307 AGGATGCTGTGGCCCTCGAGAGACAGGTGTCAAGGCAAGGATCCAGAGCCGAGGT 366
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 DB 367 CTACGCGCGCGCTCGGCGCGACGAGCGCTGAGCGCGCGCTTCCAGCGGAGAGCG 426
 QY 799 CTTCACGCGCTTCAGCCCACTATCCGATCTGACAGCAGATGACCTGCACTCCAC 858
 DB 427 CTTCACGCGCTTCAGCCCACTATCCGATCTGACAGCAGATGACCTGCACTCCAC 486
 QY 859 CATCTGCTGTCAAGCGGAGAGAGCGCCCACTACAGGCGCCCTGCACTCTCAGCT 918
 DB 487 CATCTGCTGTCAAGCGGAGAGAGCGCCCACTACAGGCGCCCTGCACTCTCAGCT 546
 QY 919 TGGGAGACCGCGAGCAGCAGCTGAATGAACCGGAGGTGAGCGCGCGCGCGCGCGCGCGCG 978
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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Perfect score: 1321
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Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1229	93.0	4839	8	ACC49552 Tumour-as
5	1229	93.0	4839	11	ADP65809 Human STA
6	1229	93.0	4839	11	ADP65729 Human tra
7	1229	93.0	4839	12	ADM67045 Human hom
8	1229	93.0	4839	13	ADR65875 Human pro
9	1229	93.0	4839	13	ADR66778 Human pro
10	1229	93.0	4839	13	ADU06063 Novel bro
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12	1227.4	92.9	1383	10	ADC37326 Nuclear f
13	909	68.8	4519	13	ADP65729 Human tra
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15	803.2	60.7	1140	6	AA75151 CDNA enco
16	802.2	60.7	1140	6	ABK92120 Prostate
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20	802.2	60.7	4527	14	ADV85880 Human ARP
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23	801.6	60.7	969	3	AA75163 CDNA cion
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ALIGNMENTS

RESULT 1
ID ABK12137 standard; CDNA; 1321 BP.

XX AC ABK12137;

DT 05-JUN-2002 (first entry)

XX DE Human CDNA encoding Mechanically Induced Vascular Receptor 1, MIVR-1.

XX KW Human; ss: gene; MIVR-1; Mechanically Induced Vascular Receptor 1;

XX KW cytosolic; cardiant; cerebroprotective; antiarteriosclerotic;

XX KW cardiac cell; anti-apoptotic; vascular endothelial cell;

XX KW heart failure.

XX OS Homo sapiens.

XX FH Key

XX CDS

XX WO200216416-A2.

XX PD 28-FEB-2002.

XX 21-AUG-2001; 2001WO-US026089.

XX PR 22-AUG-2000; 2000US-0227159P.

XX PA (BGM) BRIGHAM & WOMENS HOSPITAL INC.

XX PA (PF12) PFIZER INC.

XX PI Lee RT, Landshulz KT, Kennedy SP, Thompson JF, Turi TG;

XX DR WPI; 2002-280912/32.

XX DR P-PSDB; AAU78231.

XX PT Novel nucleic acid molecule encoding Mechanically Induced Vascular

PT Receptor-1 polypeptide, useful for treating cardiovascular diseases.

XX Claim 2; Page 87-88; 105bp; English.
PS The invention relates to an isolated nucleic acid molecule encoding a
XX Mechanically induced Vascular Receptor (MIVR)-1 polypeptide having
CC cardiac cell anti-apoptotic activity and fragments of it provided they
CC are not identical to Genbank sequences A1761441.1, A1594390, NM_004338
CC and A0177461. Also included are expression vectors, host cells, the MIVR-
CC 1 polypeptide, MIVR-1 binding peptides, modulators of MIVR-1, contacting
CC a molecule having cardiac cell anti-apoptotic activity with a candidate
CC agent, where the molecule is a nucleic acid molecule comprising MIVR-1,
CC IEX-1, VDRP-1, BFG-2 and R15-11d or its expression product, determining
CC if the anti-apoptotic activity is modulated and thereby identifying a
CC modulator. The cardiac cell anti-apoptotic molecules and nucleic acids
CC of the invention are useful for treating, diagnosing and monitoring
CC progression of such diseases and disorders as characterised by increased
CC apoptotic cell-death of vascular endothelial cells e.g. cardiac
CC hypertrophy, myocardial infarction, stroke, arteriosclerosis and heart
CC failure. The present sequence encodes human MIVR-1
XX
SQ Sequence 1321 BP; 223 A; 493 C; 440 G; 165 T; 0 U; 0 Other;
Query Match 100.0%; Score 1321; DB 6; Length 1321;
Best Local Similarity 100.0%; Pred. No. 3e-198;
Matches 1321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGACCGCGGTCCTCGAGCGAAACCGATCTCTTGGAATTGAGAGAGAGAGCGG 60
DB 1 CGACCGCGGTCCTCGAGCGAAACCGATCTCTTGGAATTGAGAGAGAGAGCGG 60
QY 61 CGGCG 120
DB 61 CGGCG 120
QY 121 GCGCGCAGCG 180
DB 121 GCGCGCAGCG 180
QY 121 GCGCGCAGCG 180
DB 121 GCGCGCAGCG 180
QY 181 ACG 240
DB 181 ACG 240
QY 241 TGAAGCG 300
DB 241 TGAAGCG 300
QY 301 CTCGCCCG 360
DB 301 CTCGCCCG 360
QY 361 CCCCAGCG 420
DB 361 CCCCAGCG 420
QY 421 CTTGATGGGGGTCAACACACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
DB 421 CTTGATGGGGGTCAACACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
QY 481 GTGCAACTGCAAAACGCTCTTTGTTCCAGAGCATGAGATCAAGAGCTGAGTTGTTCA 540
DB 481 GTGCAACTGCAAAACGCTCTTTGTTCCAGAGCATGAGATCAAGAGCTGAGTTGTTCA 540
QY 541 GATCATCATCATCTGT 600
DB 541 GATCATCATCATCTGT 600
QY 601 CCACACAAAGCTGT 660
DB 601 CCACACAAAGCTGT 660
QY 661 AGATGCTCTGTCTGT 720
DB 661 AGATGCTCTGTCTGT 720

QY 721 AATCCAGAGCGCGAGGTCATACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
DB 721 AATCCAGAGCGCGAGGTCATACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
QY 781 CTTGCGCCAGCGGAGGCTTTCACACGCTTTCAGGCCACCTATCCGTACCTGACACGA 840
DB 781 CTTGCGCCAGCGGAGGCTTTCACACGCTTTCAGGCCACCTATCCGTACCTGACACGA 840
QY 841 GATGACCTGACACCCACCATCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
DB 841 GATGACCTGACACCCACCATCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 901 CCCCTGACCCCTCAGCTTGGGAGACCCCGAGCAGCAGCTGAACTGAAACCGGAGTGT 960
DB 901 CCCCTGACCCCTCAGCTTGGGAGACCCCGAGCAGCAGCTGAACTGAAACCGGAGTGT 960
QY 961 GCGGCGACCCCGCAAAACGAACCATCTTTCAGACAGTGAACCTGATGATAGTCCAGCTGG 1020
DB 961 GCGGCGACCCCGCAAAACGAACCATCTTTCAGACAGTGAACCTGATGATAGTCCAGCTGG 1020
QY 1021 CGGCGCTGCG 1080
DB 1021 CGGCGCTGCG 1080
QY 1081 GCGGATGAGAGGCG 1140
DB 1081 GCGGATGAGAGGCG 1140
QY 1141 CTTTCAGACACAGCAGAGCAGAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
DB 1141 CTTTCAGACACAGCAGAGCAGAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
QY 1201 CACACACATGCG 1260
DB 1201 CACACACATGCG 1260
QY 1261 AGGACACCTCTCTTGAAGGTCCTCCAGAGGCGCGCGCGCGCGCGCGCGCGCGCG 1320
DB 1261 AGGACACCTCTCTTGAAGGTCCTCCAGAGGCGCGCGCGCGCGCGCGCGCGCGCG 1320
QY 1321 G 1321
DB 1321 G 1321
RESULT 2
ID AEB22787 standard; DNA; 4930 BP.
XX AEB22787;
AC 22-SEP-2005 (first entry)
XX
XX Human colon cancer-associated gene SEQ ID NO:82.
XX cancer; genetic marker; lymphoma; cytostatic; hematological disease;
XX immune disorder; neoplasm; colon tumor; gastrointestinal disease;
XX adenocarcinoma; carcinoma; screening; diagnostic; prognostic;
XX pharmaceutical; ds; gene.
OS Homo sapiens.
XX
XX WO2005064009-A1.
PN 14-JUL-2005.
PD
XX
XX 23-DEC-2004; 2004MO-DK00914.
PP
XX 27-DEC-2003; 2003DK-00001940.
PR 24-JAN-2004; 2004DK-0000096.
PR 07-APR-2004; 2004DK-0000086.
PR 26-NOV-2004; 2004DK-00001843.

XX 18-NOV-2004 (first entry)
 DT Tumour-associated antigenic target (TAT) cDNA DNa326860, SEQ ID NO:5823.
 DE
 XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
 KM tumour; diagnosis; cell proliferative disorder; breast cancer;
 KM colorectal cancer; lung cancer; ovarian cancer; liver cancer;
 KM central nervous system cancer; bladder cancer; pancreatic cancer;
 KM cervical cancer; melanoma; leukemia; hybridisation probe;
 KM chromosome identification; chromosome mapping; gene mapping;
 KM gene therapy; cytostatic; gene; ss.
 XX
 OS Homo sapiens.
 PN MO204030615-A2.
 XX
 PD 15-APR-2004.
 XX
 PE 29-SEP-2003; 2003WO-US028547.
 XX
 PR 02-OCT-2002; 2002US-0414971P.
 PA (GENTH) GENENTECH INC.
 XX
 PI Wu TD, Zhang Z, Zhou Y;
 XX WPI, 2004-347921/32.
 DR
 XX New tumor-associated antigenic target polypeptides and nucleic acids,
 PT useful in preparing a medicament for treating or detecting a
 PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 PT prostate cancer or tumor.
 PT
 XX Claim 1; SEQ ID NO 5823; 7273bp; English.
 XX
 XX The invention relates to human tumour-associated antigenic target (TAT)
 CC polypeptides, and their related nucleic acids. The TAT polypeptides are
 CC overexpressed in cancer tissues compared to normal tissues, and may thus
 CC serve as effective targets for the diagnosis and treatment of cancer in
 CC mammals. The invention also relates to nucleic acid and polypeptide
 CC sequences at least 80% identical to the TAT nucleic acid and
 CC polypeptides; expression vectors and host cells comprising a TAT nucleic
 CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
 CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
 CC TAT polypeptide; and methods and compositions for the treatment or
 CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
 CC antibodies, antagonists, binding molecules and compositions are useful
 CC for diagnosing or treating a cell proliferative disorder associated with
 CC increased TAT expression, particularly cancers such as breast cancer,
 CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
 CC cancer, pancreatic cancer, cervical cancer, cancers of the central
 CC nervous system, melanoma and leukemia. TAT nucleic acids may further be
 CC used as hybridisation probes, in chromosome and gene mapping, in
 CC chromosome identification and in gene therapy. The present sequence
 CC represents a TAT nucleic acid of the invention
 CC
 XX
 SQ Sequence 4911 BP; 1114 A; 1331 C; 1324 G; 1142 T; 0 U; 0 Other;
 Query Match 98.5%; Score 1301; DB 13; Length 4911;
 Best Local Similarity 100.0%; Pred. No. 3.7e-195;
 Matches 1301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 121 TGCAGCCATTTTCGAGCGCCAGCCGCGGCACTGCGACGCCCCCGGGGCTGCCAG 180
 Qy 201 GGGAGGCGGGGGGGGGCGCAGCGGAGCGGCTCCCGGCACTGAGCCCCCGGGGCCCCGG 260
 Db 181 GGGAGGCGGGGGGGGGCGCAGCGGAGCGGCTCCCGGCACTGAGCCCCCGGGGCCCCGG 240
 Qy 261 GAACCTTGGCGGACCCGAGCCCGGAGCGGGGGCGGCTCCCGGCGGCGGCTCC 320
 Db 241 GAACCTTGGCGGACCCGAGCCCGGAGCGGGGGCGGCTCCCGGCGGCGGCTCC 300
 Qy 321 TGATGCGGGGGCCCACTGCTCGGCGCGGAGCGGAGCGGCGGCGGCGGCGGCGGCGG 380
 Db 301 TGATGCGGGGGCCCACTGCTCGGCGCGGAGCGGAGCGGCGGCGGCGGCGGCGGCGG 360
 Qy 381 CCG 440
 Db 361 CCG 420
 Qy 441 CCG 500
 Db 421 CCG 480
 Qy 501 TGTTCAGAGCATGAGATGACGAGCTGAGTTTGTTCAGATCATCATCTGCTGGTGG 560
 Db 481 TGTTCAGAGCATGAGATGACGAGCTGAGTTTGTTCAGATCATCATCTGCTGGTGG 540
 Qy 561 TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 620
 Db 541 TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 Qy 621 GATCTCTCATCAGCGCGGCGCAGCGCGGGGCGGAGAGAGATGCGCTTCTCAGAG 680
 Db 601 GATCTCTCATCAGCGCGGCGCAGCGGGGCGGAGAGAGATGCGCTTCTCAGAG 660
 Qy 681 GATGCTGTGAGCTCTCGAGAGCAGATGTCAGGCAAGCAATCCAGAGCCCGAGGCT 740
 Db 661 GATGCTGTGAGCTCTCGAGAGCAGATGTCAGGCAAGCAATCCAGAGCCCGAGGCT 720
 Qy 741 ACGGCGCGCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 800
 Db 721 ACGGCGCGCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
 Qy 801 TCCAGCGCTTCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 860
 Db 781 TCCAGCGCTTCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840
 Qy 861 TCTGCTGTGAGAGGGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 920
 Db 841 TCTGCTGTGAGAGGGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 900
 Qy 921 GGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 980
 Db 901 GGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 960
 Qy 981 CCATCTTCAGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1040
 Db 961 CCATCTTCAGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
 Qy 1041 GTAACCTGGGATGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1100
 Db 1021 GTAACCTGGGATGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1080
 Qy 1101 CCACCTTACAGGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTAT 1160
 Db 1081 CCACCTTACAGGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTAT 1140
 Qy 1161 GTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1220
 Db 1141 GTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1200
 Qy 1221 AGAGCGAGCGCATCTGAGAGCAAGAGAGATTAACAGAAAGACACCTCTTAAAGGCTC 1280
 Db 1201 AGAGCGAGCGCATCTGAGAGCAAGAGAGATTAACAGAAAGACACCTCTTAAAGGCTC 1260

QY 1281 CCCAGGGGGCCGCGCTGCGTGTGCTAGTGAAGGACAG 1321
 DB 1261 CCCAGGGGGCCGCGCTGCGTGTGCTAGTGAAGGACAG 1301
 RESULT 4
 ACC49552
 ID ACC49552 standard; cDNA; 4839 BP.
 XX ACC49552;
 AC ACC49552;
 DT 01-JUL-2003 (first entry)
 DE Tumour-associated antigenic target protein TAT379 SEQ ID NO:119.
 XX Human; tumour-associated antigenic target; TAT; tumour; diagnosis;
 KW cancer; gene; ss.
 XX Homo sapiens.
 OS WO2003024392-A2.
 PN 27-MAR-2003.
 XX 11-SEP-2002; 2002MO-US028859.
 PF 18-SEP-2001; 2001US-0323268P.
 XX 19-OCT-2001; 2001US-0339227P.
 PR 07-NOV-2001; 2001US-0336827P.
 PR 20-NOV-2001; 2001US-0331906P.
 PR 02-JAN-2002; 2002US-034544P.
 PR 03-APR-2002; 2002US-0369724P.
 PR 19-AUG-2002; 2002US-0404809P.
 XX (GENE) GENENTECH INC.
 PA Frantz G, Hillan KJ, Phillips HS, Polakis P, Spencer SD;
 PI Williams PM, Wu TD, Zhang Z;
 XX MPI: 2003-354551/3.
 DR P-PSDB; ABP97234.
 XX New antibodies against tumor-associated antigenic target polypeptide,
 PT useful for treating or diagnosing tumors or cancers in mammals, e.g.
 PT prostate cancer, lung cancer, prostate adenocarcinomas or renal cell
 PT carcinomas.
 XX Claim 2; Fig 119; 285bp; English.
 PS ACC49493 to ACC49552 encode the human tumour-associated antigenic target
 CC (TAT) proteins given in ABP97175 to ABP97234. The present invention
 CC describes an isolated antibody that binds to a polypeptide having at
 CC least 80 % sequence identity to any of the 60 150-800 residue amino acid
 CC sequences (S1), given in ABP97175 to ABP97234, comprising (S1), lacking
 CC its associated signal peptide, encoded by any of the 60 2000-3000 base
 CC pair sequences (S2), given in ACC49493 to ACC49552. TAT proteins have
 CC cytotoxic activity. The antibody can be used for treating or diagnosing
 CC tumours or cancers in mammals, e.g. prostate cancer, lung cancer, breast
 CC cancer, colon cancer, ovarian cancer, prostate adenocarcinomas, renal
 CC cell carcinomas, or thyroid cancer.
 CC
 SQ Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;
 Query Match 93.0%; Score 1229; DB 8; Length 4839;
 Best Local Similarity 100.0%; Pred. No. 7, 2e-184;
 Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 93 GGAAGCTAGCGGACAGAGGCTCAGCCCGCGGACGCGCGCGCTGCGACGCCATT 152
 DB 1 GGAAGCTAGCGGACAGAGGCTCAGCCCGCGGACGCGCGCGCTGCGACGCCATT 60
 QY 153 TTCGAGACGACCCCGCGGACACTGCGGACGCGCGCGCGCTGCGAGGGAGGCCGGG 212

DB 61 TTCGAGACGACCCCGCGGACACTGCGGACGCCCGCGGCGCTGCGAGGGAGGCCCGGG 120
 QY 213 GGGCGCAGCGGAGCGCGGCTCCCGGCACTGAGCCCGCGCGCGCGGGAACCTTGGCGGC 272
 DB 121 GGGCGCAGCGGAGCGCGGCTCCCGGCACTGAGCCCGCGCGCGCGGGAACCTTGGCGGC 180
 QY 273 GACCCGAGCCCGCGGAGCGCGGCGCGCTCCCGCGCGCGCGCGCTTGTGATCGCGGC 332
 DB 181 GACCCGAGCCCGCGGAGCGCGGCGCGCTCCCGCGCGCGCGCGCTTGTGATCGCGGC 240
 QY 333 CCCAGCTCCGGGACGCGCGCGGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 392
 DB 241 CCCAGCTCCGGGACGCGCGCGGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
 QY 393 GCGCGCGCGCGCGCGCGCTTGTGATGAGGGGCTTAAGACGCGCGCGCGCGCGCGCGCG 452
 DB 301 GCGCGCGCGCGCGCGCGCTTGTGATGAGGGGCTTAAGACGCGCGCGCGCGCGCGCGCG 360
 QY 453 CCGCGCGCGGACCGCAATGTCTCTGCAAGTCACTGCAAGCTCTTGTTCAGAGCA 512
 DB 361 CCGCGCGGACCGCAATGTCTCTGCAAGTCACTGCAAGCTCTTGTTCAGAGCA 420
 QY 513 TGGAGATCAGGAGCTGAGATTGTTCAGATCATCATCATCTGTGTGTGATGATGTGA 572
 DB 421 TGGAGATCAGGAGCTGAGATTGTTCAGATCATCATCATCTGTGTGTGATGATGTGA 480
 QY 573 TGTGTGTGTGATCATCTGTCTGTGAGCCACTCAAGCTCTTGTGCAAGCTCTTGTGATCA 632
 DB 481 TGTGTGTGTGATCATCTGTCTGTGAGCCACTCAAGCTCTTGTGCAAGCTCTTGTGATCA 540
 QY 633 GCGCGCAGCGCAGGGGCGGAG 692
 DB 541 GCGCGCAGCGCAGGGGCGGAG 600
 QY 693 CCTCGAGAGACAGTGTCAAGCAACGGAATCCAGAGCCGCGAGCTTACGCCCGCGCTC 752
 DB 601 CCTCGAGAGACAGTGTCAAGCAACGGAATCCAGAGCCGCGAGCTTACGCCCGCGCTC 660
 QY 753 GCGCCACCGCGCGCTGCG 812
 DB 661 GCGCCACCGCGCGCTGCG 720
 QY 813 AGCCCACTATCCGACTGCTGAGACGAGATCGACCTTGCACCCACCATCTCGCTGTAG 872
 DB 721 AGCCCACTATCCGACTGCTGAGACGAGATCGACCTTGCACCCACCATCTCGCTGTAG 780
 QY 873 ACGGGAGAGACCCCGACCTTACAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 932
 DB 781 ACGGGAGAGACCCCGACCTTACAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
 QY 933 AGCAGCTGAACCTGAACCGGAGTGTGTCGCGGACCCCGCAAGAACCATCTTTCGACA 992
 DB 841 AGCAGCTGAACCTGAACCGGAGTGTGTCGCGGACCCCGCAAGAACCATCTTTCGACA 900
 QY 993 GTGACCTGATGATGTGTCCAGAGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1052
 DB 901 GTGACCTGATGATGTGTCCAGAGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
 QY 1053 TCAGGCGCACGCTGACAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1112
 DB 961 TCAGGCGCACGCTGACAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1020
 QY 1113 AGGTATGCGGACCTTACCCGCGGCTCTCTTTCAGACCAAGACAGAGAGAGAGAGAGAGAG 1172
 DB 1021 AGGTATGCGGACCTTACCCGCGGCTCTCTTTCAGACCAAGAGAGAGAGAGAGAGAGAG 1080
 QY 1173 CTTTCTGAGAGAGAGCGCGGCTTCCACACACACATGCGCGCGCTTAGAGAGCGAGGCA 1232
 DB 1081 CTTTCTGAGAGAGAGCGCGGCTTCCACACACACATGCGCGCGCTTAGAGAGCGAGGCA 1140
 QY 1233 TCTGAGACAAAGAGAGATTAACAGAAAGACACCTCTCTAGGCTCCCAAGGGGGGCGC 1292

Db 1141 TCTGAGCAAGAGAGATAACAGAAAGACACCTCTCTAGGGTCCCAAGGAGGACC 1200

QY 1293 GGGCTGGGGCTGCTGAGGTGAAAAGCAG 1321

Db 1201 GGGCTGGGGCTGCTGAGGTGAAAAGCAG 1229

RESULT 5

ADP65809

ID ADP65809 standard; DNA; 4839 BP.

AC ADP65809;

XX 12-AUG-2004 (first entry)

DE Human STAG1/PMEPA1 mRNA, complete cds DNA.

XX autoimmune disease; arthritis; gene expression analysis;

KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;

KW antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;

KW immunomodulatory; lupus; ankylosing spondylitis; fibrositis;

KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;

KW immune; ds; human.

XX Homo sapiens.

XX WO2003072827-A1.

PN 04-SEP-2003.

PD 31-OCT-2002; 2002MO-US035433.

XX 31-OCT-2001; 2001US-0336220P.

PR (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

XX Hirsch R, Thornton SL;

PI WPI; 2003-712740/67.

XX GENBANK; AF305616.

DR

XX Diagnosing and analyzing autoimmune disease using gene expression

PT profiles and microarray technology, useful for diagnosing and treating

PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and

PT gout.

PS Disclosure; Page; 56pp; English.

XX The invention relates to a novel method for diagnosing and analyzing

CC autoimmune disease or arthritides. The method comprises obtaining a

CC patient sample containing mRNA, analyzing gene expression using the mRNA

CC that results in a gene expression signature of the mRNA, and using that

CC gene expression signature to diagnose or analyse the autoimmune disease

CC or arthritides in the patient, where gene expression of at least 60% of

CC the genes correlates with that of the gene signature. The invention

CC further comprises a treatment of rheumatoid arthritis; identification of

CC genes for targeting in the treatment of rheumatoid arthritis in a mammal

CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an

CC array or gene chip, specific for rheumatoid arthritis; diagnosis or

CC analysis of autoimmune disease or rheumatoid arthritis; screening the

CC efficacy of a candidate drug in vitro for the treatment of collagen-

CC induced arthritis; and reducing the symptoms associated with collagen-

CC induced arthritis. The compositions of the invention have the following

CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,

CC antigout, antiinflammatory, dermatological, and immunomodulatory. The

CC methods and compositions of the present invention are useful for

CC diagnosing and treating autoimmune disease or arthritides, such as

CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,

CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an

CC immune disease caused by an infectious agent. This polynucleotide

CC represents a DNA sequence relating to the genes used in the analysis and

CC treatment of autoimmune diseases or arthritides. Note: This sequence is

CC not shown in the specification. It has been supplied in an electronic

CC format from WIFO.

XX Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;

SO Query Match 93.0%; Score 1229; DB 11; Length 4839;

Best Local Similarity 100.0%; Pred. No. 7,2e-184;

Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 GGAAGCTAGCGGAGAGAGGCTCAGCCCGCGGAGAGGCGCGCGCTGCGAGCCATT 152

Db 1 GGAAGCTAGCGGAGAGAGGCTCAGCCCGCGGAGAGGCGCGCGCTGCGAGCCATT 60

QY 153 TTCGAGAGCCAGCCCGGAGAGGCTGCGAGAGCCCGGAGAGGCGGAGAGGCGGAG 212

Db 61 TTCGAGAGCCAGCCCGGAGAGGCTGCGAGAGCCCGGAGAGGCGGAGAGGCGGAG 120

QY 213 GGGGAGAGGAGAGGCGGCTCCCGGAGAGGAGCCCGGAGAGGCGGAGAGGCGGAG 272

Db 121 GGGGAGAGGAGAGGCGGCTCCCGGAGAGGAGCCCGGAGAGGCGGAGAGGCGGAG 180

QY 273 GAGCCGAGCCCGGAGAGGCGGAGGCGGCGCTCCCGGAGAGGCGGAGAGGCGGAG 332

Db 181 GAGCCGAGCCCGGAGAGGCGGAGGCGGCGCTCCCGGAGAGGCGGAGAGGCGGAG 240

QY 333 CCGAGCTCCGAGAGGCGGAGAGGCGGAGAGGCGGAGAGGCGGAGAGGCGGAGAGG 392

Db 241 CCGAGCTCCGAGAGGCGGAGAGGCGGAGAGGCGGAGAGGCGGAGAGGCGGAGAGG 300

QY 393 GCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAG 452

Db 301 GCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAG 360

QY 453 CCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAG 512

Db 361 CCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAG 420

QY 513 TGAGATCAGGAGGCTGAGGTTGTTGATCATCATCATCATCATCATCATCATCATCAT 572

Db 421 TGAGATCAGGAGGCTGAGGTTGTTGATCATCATCATCATCATCATCATCATCATCAT 480

QY 573 TGAGTGTGTGATCAGGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 632

Db 481 TGAGTGTGTGATCAGGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540

QY 633 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 692

Db 541 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600

QY 693 CCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 752

Db 601 CCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660

QY 753 GGGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 812

Db 661 GGGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720

QY 813 AGCCCACTTATCCTGATCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 872

Db 721 AGCCCACTTATCCTGATCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780

QY 873 AGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 932

Db 781 AGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840

QY 933 AGGAGCTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAA 992

Db 841 AGGAGCTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAA 900

QY 993 GTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1052

Db 901 GTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960

QY 1053 TCAGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1112

DB 961 TCAGGCCACGCTGCTACGCGACGCGCGCGCATGAGAGGCGCGCGCCGACCTTACAGCG 1020
 QY 1113 AGGTGATCGGCGACCTACCGCGGGGTCTCTCTTCAGCACCGACGAGAGAGTGCGCGCTT 1172
 DB 1021 AGGTATCGGCGACCTACCGCGGGGTCTCTCTTCAGCACCGACGAGAGAGTGCGCGCTT 1080
 QY 1173 CCTTGTGAGAGGAGACCGCGCTTCACACACACACATCGCGCGCTTATAGAGCGGAGCA 1232
 DB 1081 CCTTGTGAGAGGAGACCGCGCTTCACACACACACATCGCGCGCTTATAGAGCGGAGCA 1140
 QY 1233 TCTGAGCAAGAGAGATTAACAGAAAGACACCGCTCTAGAGGTCGCCAGGCGCGCC 1292
 DB 1141 TCTGAGCAAGAGAGATTAACAGAAAGACACCGCTCTAGAGGTCGCCAGGCGCGCC 1200
 QY 1293 GGGCTGCGGCTGCTAGTGAAGGAGCAG 1321
 DB 1201 GGGCTGCGGCTGCTAGTGAAGGAGCAG 1229

RESULT 6
 ADP65729
 ID ADP65729 standard; DNA; 4839 BP.
 AC ADP65729;
 DT 12-AUG-2004 (first entry)
 DE Human transmembrane, prostate androgen induced RNA (TMEMPA1), DNA.
 KM autoimmune disease; arthritis; gene expression analysis;
 KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
 KW antiarthritis; osteopathic; antigen; antiinflammatory; dermatological;
 KW immunomodulatory; lupus; ankylosing spondylitis; fibrositis;
 KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
 KW immune; ds; human.
 OS Homo sapiens.
 PN MO2003072827-A1.
 PD 04-SEP-2003.
 PF 31-OCT-2002; 2002WO-US035433.
 PR 31-OCT-2001; 2001US-0336220P.
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 PI Hirsch R, Thorton SL;
 DR WPI; 2003-712740/67.
 DR GENBANK; NM_020182.
 PT Diagnosing and analyzing autoimmune disease using gene expression
 PT profiles and microarray technology, useful for diagnosing and treating
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
 PT gout.
 PS Disclosure; Page; 56pp; English.

The invention relates to a novel method for diagnosing and analyzing
 CC autoimmune disease or arthritides. The method comprises obtaining a
 CC patient sample containing mRNA, analyzing gene expression using the mRNA
 CC that results in a gene expression signature of the mRNA, and using that
 CC gene expression signature to diagnose or analyse the autoimmune disease
 CC or arthritides in the patient, where gene expression of at least 60% of
 CC the genes correlates with that of the gene signature. The invention
 CC further comprises a treatment of rheumatoid arthritis; identification of
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal;
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
 CC analyses of autoimmune disease or rheumatoid arthritis; screening the

CC efficacy of a candidate drug in vitro for the treatment of collagen-
 CC induced arthritis; and reducing the symptoms associated with collagen-
 CC induced arthritis. The compositions of the invention have the following
 CC activities: immunosuppressive, antirheumatic, antiarthritis, osteopathic,
 CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
 CC method and compositions of the present invention are useful for
 CC diagnosing and treating autoimmune disease or arthritides, such as
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
 CC immune disease caused by an infectious agent. This polynucleotide
 CC represents a DNA sequence relating to the genes used in the analysis and
 CC treatment of autoimmune diseases or arthritides. Note: This sequence is
 CC not shown in the specification. It has been supplied in an electronic
 CC format from WIPO.

SQ Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;

Query Match 93.0%; Score 1229; DB 11; Length 4839;
 Best Local Similarity 100.0%; Pred. No. 7.2e-184;
 Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 GGAAGCTAGCGGAGAGGCTCAGCCCGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 152
 DB 1 GGAAGCTAGCGGAGAGGCTCAGCCCGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 60
 QY 153 TTCCGAGAGCCACCGCGGCGGACCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 212
 DB 61 TTCCGAGAGCCACCGCGGCGGACCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
 QY 213 GGGCGCAGCGAGCGCGGTCGCGGCACTGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCG 272
 DB 121 GGGCGCAGCGAGCGCGGTCGCGGCACTGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCG 180
 QY 273 GACCCGAGCCCGGCGAGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 332
 DB 181 GACCCGAGCCCGGCGAGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
 QY 333 CCCGCTCGGCGCGCGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 392
 DB 241 CCCGCTCGGCGCGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
 QY 393 GCGCGCGCGCGCGCGGCTGCAATGACCGCTTGATGGGGGTCAACAGCACCGCGCGCGCG 452
 DB 301 GCGCGCGCGCGCGCGGCTGCAATGACCGCTTGATGGGGGTCAACAGCACCGCGCGCGCG 360
 QY 453 CGCGCGCGCGCGCGCAATGCTCTGCGACGTGCACTGCAAAAGCTTTGTTCCAGAGCA 512
 DB 361 CGCGCGCGCGCGCGCAATGCTCTGCGACGTGCACTGCAAAAGCTTTGTTCCAGAGCA 420
 QY 513 TGGAGATCAGGAGCTGAGAGTTGTTCAAGATCATCATGCTGGTGGATGATGGTGA 572
 DB 421 TGGAGATCAGGAGCTGAGAGTTGTTCAAGATCATCATGCTGGTGGATGATGGTGA 480
 QY 573 TGGTGGTGGTATCAGTGCTGCTGAGCACTAACAAGTGTCTGACAGGTCCTTCATCA 632
 DB 481 TGGTGGTGGTATCAGTGCTGCTGAGCACTAACAAGTGTCTGACAGGTCCTTCATCA 540
 QY 633 GCGCGCACGCGAGGGGCGAGAGAGAAATGCTGTCTCAGAGAGATCCTGTGGC 692
 DB 541 GCGCGCACGCGAGGGGCGAGAGAGAAATGCTGTCTCAGAGAGATCCTGTGGC 600
 QY 693 CTTGAGAGAGCAAGTGTACAGGCAACGGAATCCGAGACCGGAGGTCTACGCGCGCGCTC 752
 DB 601 CTTGAGAGAGCAAGTGTACAGGCAACGGAATCCGAGACCGGAGGTCTACGCGCGCGCTC 660
 QY 753 GGGCGACGAGCGCGCTGGCGCGTGGCGCGCTTGCAGGAGGAGGCTTCCACGCGCTTC 812
 DB 661 GGGCGACGAGCGCGCTGGCGCGTGGCGCGCTTGCAGGAGGAGGCTTCCACGCGCTTC 720
 QY 813 AGCCCACTATCGTACTGACAGCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 872
 DB 721 AGCCCACTATCGTACTGACAGCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 780


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Db 721 AGCCCACTATCCGTAATCGAGACAGATCGACTGCAACCACTTCGCTGTGAG 780
Oy 873 ACGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 932
Db 781 ACGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Oy 933 AGCAGCTGAACTGAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 992
Db 841 AGCAGCTGAACTGAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Oy 993 GTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1052
Db 901 GTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
Oy 1053 TCAGGCGCAGCGTGTACAGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1112
Db 961 TCAGGCGCAGCGTGTACAGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1020
Oy 1113 AGGTGATGCGGCGTGTACAGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1172
Db 1021 AGGTGATGCGGCGTGTACAGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1080
Oy 1173 CTTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1232
Db 1081 CTTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Oy 1233 TCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1292
Db 1141 TCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
Oy 1293 GGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1321
Db 1201 GGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1229

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RESULT 8
ADRS65875
ID ADRS65875 standard; DNA; 4839 BP.

AC ADRS65875;

DT 02-DEC-2004 (first entry)

DE Human prostatic carcinoma derived DNA SEQ ID 71 #1.

XX human, cytostatic; diagnosis; prostatic cancer;

KM differential expression analysis; de.

OS Homo sapiens.

PN WO2004076614-A2.

PD 10-SEP-2004.

PF 22-FEB-2004; 2004WO-DE000433.

PR 27-FEB-2003; 2003DE-0100985.

PR 14-MAY-2003; 2003DE-01022134.

PA (HINZ/) HINZMANN B.

PA (DAHL/) DAHL E.

PA (ROSE/) ROSENTHAL A.

PA (HERN/) HERMANN K.

PA (PILA/) PILARSKY C.

PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarczyk C, Specht T;

PI Schmitt A, Beckmann G, Brumendorf T, Kinnemann H, Roepke S;

PI Kinzhong L, Staub E;

XX WPI; 2004-653386/63.

XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,

PT useful for diagnosis, treatment and in screening for specific binding
agents.

XX Claim 1; Page 277; 1607pp; German.

PS This invention describes novel cytostatic polynucleotide and polypeptide
sequences which can be used in a method for diagnosing prostatic cancer
or the risk of developing prostatic cancer. Diagnosis is based on
determining over transcription or over expression of the sequences in
prostatic tissue. Screening for inhibitors of the sequences or detection
of substances involves a binding assay, any compounds that bind are
selected, optionally after deconvolution of mixtures. Detection of a
predetermined minimum level of the reporter indicates the presence of
tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
short-interfering RNA or ribozymes, an organic molecule of molecular
weight below 5000, preferably 300, that binds to the polypeptide; an
aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
polypeptide, preferably humanised or human; an anti-Idiotypic, non-human
(monoclonal) antibody directed against Ab or any of the above derivatised
with a reporter group, cell toxin, immunostimulatory molecules and/or
radioisotope. The polynucleotides are identified in human prostatic
cancer by differential expression analysis, using DNA microarrays,
between normal and tumorous tissues, with (over)expression being detected
by quantitative PCR. Analysis of prostatic cancer samples showed that
CD24 was upregulated in many of them. Sections of tissue, isolated from
prostatic cancer patients, or subjects at risk, were incubated
sequentially with anti-human CD4 murine monoclonal antibodies;
biotinylated second antibody; streptavidin-conjugated horseradish
peroxidase and then diaminobenzidine as colour former (brown). The
samples were counterstained with hemalum (blue). Malignant cells stained
strongly but non-malignant cells only weakly. In 15 of 63 samples of
adenocarcinoma, membrane and cytoplasmic staining was very strong, and
lymph node metastases were also stained. ADRS65805-ADR66954 represent the
polynucleotide and polypeptide sequences used in the method of the
invention.

CC Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;

XX Query Match 93.0%; Score 1229; DB 13; Length 4839;

XX Best Local Similarity 100.0%; Pred. No. 7.2e-184;

XX Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy 93 GAAAAGTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 152
Db 1 GAAAAGTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
Oy 153 TTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 212
Db 61 TTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Oy 213 GGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 272
Db 121 GGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Oy 273 GACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 332
Db 181 GACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Oy 333 CCAAGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 392
Db 241 CCAAGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Oy 393 GCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 452
Db 301 GCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Oy 453 CCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 512
Db 361 CCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Oy 513 TGAAGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 572
Db 421 TGAAGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480

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QY 573 TGGTGTGTGTATCATCGTGTCTGCTGAGCCACTACAGCTGTCTGCAAGCGTCTTCATCA 632
 DB 481 TGGTGTGTGTATCATCGTGTCTGCTGAGCCACTACAGCTGTCTGCAAGCGTCTTCATCA 540
 QY 633 GCCCGCAGCGAGCGAGCGAGAGAGAAAGATGCGCTCTCTCCAGAAAGATGCGTGTGC 692
 DB 541 GCCCGCAGCGAGCGAGCGAGAGAGAAAGATGCGCTCTCTCCAGAAAGATGCGTGTGC 600
 QY 693 CCTCGAGAGCAGCATGTCTCAGGCAACGGAATCCAGAGCCGCAAGGTCTACGCCCCGCTC 752
 DB 601 CCTCGAGAGCAGCATGTCTCAGGCAACGGAATCCAGAGCCGCAAGGTCTACGCCCCGCTC 660
 QY 753 GGGCCACCGACCGCTGGCGCGCTGCGCCCTTTCGCCACCGGAGAGGCTTCCACCGCTTCC 812
 DB 661 GGGCCACCGACCGCTGGCGCGCTGCGCCCTTTCGCCACCGGAGAGGCTTCCACCGCTTCC 720
 QY 813 AGCCCACTATCCGTAACCTGACAGCAGAGATGACCTTGCACCCACATCTCGTGTGAG 872
 DB 721 AGCCCACTATCCGTAACCTGACAGCAGAGATGACCTTGCACCCACATCTCGTGTGAG 780
 QY 873 AGCGGAGAGAGCGCCCGACCTTACAGAGGCGCCCTGACCGCTTCAGGAGACCCCGAGC 932
 DB 781 AGCGGAGAGAGCGCCCGACCTTACAGAGGCGCCCTGACCGCTTCAGGAGACCCCGAGC 840
 QY 933 AGCAGCTGGAATCTGAACCGGAGAGTGTGTGCGGCAACCCCGCAACAGAACTTTCCACA 992
 DB 841 AGCAGCTGGAATCTGAACCGGAGAGTGTGTGCGGCAACCCCGCAACAGAACTTTCCACA 900
 QY 993 GTGACCTGATGATGT 1052
 DB 901 GTGACCTGATGATGT 960
 QY 1053 TCAGCGCCACGCTGTACAGCAGCGAGCGGCGCGATGAGAGGCGCGCGCCCACTTACAGCG 1112
 DB 961 TCAGCGCCACGCTGTACAGCAGCGAGCGGCGCGATGAGAGGCGCGCGCCCACTTACAGCG 1020
 QY 1113 AGGTATATGGCCACTACCCCGGGGTCTCTCTTTCAGACACAGAGAGAGTGTGTGTGTGT 1172
 DB 1021 AGGTATATGGCCACTACCCCGGGGTCTCTCTTTCAGACACAGAGAGAGTGTGTGTGTGT 1080
 QY 1173 CTTTGTGAGAGGAGCGCGGCTCCACACACACATGCGCCCTTACAGAGCGAGCGCA 1232
 DB 1081 CTTTGTGAGAGGAGCGCGGCTCCACACACACATGCGCCCTTACAGAGCGAGCGCA 1140
 QY 1233 TCTGAGCAGAAAGAGATTAACAGAAAGAGACACCTCTCTTACGGGTCCCAAGGGGGCC 1292
 DB 1141 TCTGAGCAGAAAGAGATTAACAGAAAGAGACACCTCTCTTACGGGTCCCAAGGGGGCC 1200
 QY 1293 GGGCTGGGGCTGCTGAGTGAAGAAAGCGAG 1321
 DB 1201 GGGCTGGGGCTGCTGAGTGAAGAAAGCGAG 1229

RESULT 9
 ADR66778
 ID ADR66778 standard; DNA; 4839 BP.

XX ADR66778;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Human prostatic carcinoma derived DNA SEQ ID 71 #4.
 XX
 KW human; cytostatic; diagnosis; prostatic cancer;
 XX differential expression analysis; ds.
 OS Homo sapiens.
 XX
 PN WO2004076614-A2.
 XX
 PD 10-SEP-2004.
 XX

PF 22-FEB-2004; 2004WO-DE000433.
 XX
 ER 27-FEB-2003; 2003DE-01009985.
 PR 14-MAY-2003; 2003DE-01022134.
 XX
 PA (HINZ/) HINZMANN B.
 PA (DAHL/) DAHL E.
 PA (ROSE/) ROSENTHAL A.
 PA (HERM/) HERMANN K.
 PA (PILAI/) PILARSKY C.
 PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarczyk C, Specht T,
 PI Schmitz A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S,
 PI Xinzhong L, Staub E;
 XX
 DR WPI; 2004-653386/63.
 XX
 PT New nucleic acids, and encoded proteins, from prostatic cancer tissue,
 PT useful for diagnosis, treatment and in screening for specific binding
 PT agents.
 XX
 PS Claim 1; Page 1447; 1607pp; German.
 XX
 CC This invention describes novel cytosolic polynucleotide and polypeptide
 CC sequences which can be used in a method for diagnosing prostatic cancer
 CC or the risk of developing prostatic cancer. Diagnosis is based on
 CC determining over transcription or over expression of the sequences in
 CC prostatic tissue. Screening for inhibitors of the sequences or detection
 CC substances involves a binding assay; any compounds that bind are
 CC selected, optionally after deconvolution of mixtures. Detection of a
 CC predetermined minimum level of the reporter indicates the presence of
 CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
 CC short-interfering RNA or ribozymes; an organic molecule of molecular
 CC weight below 5000, preferably 300, that binds to the polypeptide; an
 CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
 CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human
 CC (monoclonal) antibody directed against Ab or any of the above derivatised
 CC with a reporter group, cell toxin, immunostimulatory molecules and/or
 CC radioisotope. The polynucleotides are identified in human prostatic
 CC cancer by differential expression analysis, using DNA microarrays,
 CC between normal and tumorous tissues, with (over)expression being detected
 CC by quantitative PCR. Analysis of prostatic cancer samples showed that
 CC CD24 was upregulated in many of them. Sections of tissue, isolated from
 CC prostatic cancer patients, or subjects at risk, were incubated
 CC sequentially with anti-human CD4 murine monoclonal antibodies;
 CC biotinylated second antibody; streptavidin-conjugated horseradish
 CC peroxidase and then diaminobenzidine as colour former (brown). The
 CC samples were counterstained with hemalum (blue). Malignant cells stained
 CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
 CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
 CC lymph node metastases were also stained. ADR65805-ADR66554 represent the
 CC polynucleotide and polypeptide sequences used in the method of the
 CC invention.
 XX
 SQ Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;
 XX
 Query Match 93.0%; Score 1229; DB 13; Length 4839;
 Best Local Similarity 100.0%; Pred. No. 7, 2e-184;
 Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 93 GGAAGCTAGCGGAGAGGCTCAGCCCGGAGGAGCGCGCGCGCTGCGAGGAGCGCGG 152
 DB 1 GGAAGCTAGCGGAGAGGCTCAGCCCGGAGGAGCGCGCGCGCTGCGAGGAGCGCGG 60
 QY 153 TTCCGAGCGCCACCGCGGAGCTGCGGAGCGCCCGGAGCTGCGGAGGAGCGCGG 212
 DB 61 TTCCGAGCGCCACCGCGGAGCTGCGGAGCGCCCGGAGCTGCGGAGGAGCGCGG 120
 QY 213 GGGCGAGCGGAGCGGCTCCCGGCACTGAGCCCGCGGCGCCCGGAGAACTTTGCGGC 272
 DB 121 GGGCGAGCGGAGCGGCTCCCGGCACTGAGCCCGCGGCGCCCGGAGAACTTTGCGGC 180
 QY 273 GACCCGAGCGCGGAGCGGCGCGCGCTCCCGCGCGCGCGCTCTGATGCGGCGC 332

Db	181	GACCCGAGCCCGGCGAGCCCGGGGCGCGCTCCCCCGCGCGCGCTCTCGATGCGGGGC	240
Qy	333	CCAGACTCCGGGCGCGCGGCGGAGCGCCCCCGCGCGCTCCCGAGCCCCCGCGCGCGC	392
Db	241	CCGAGCTCCGGGCGCGCGGAGCGCCCCCGCGCGCTCCCGAGCCCCCGCGCGCGC	300
Qy	393	GGCCCGCGCGCGCGCGCTGCATGCAACCGCTGATGGGGGTGAACAACAACCGCGCGCGG	452
Db	301	GGCGGCGCGCGCGCTGCATGCAACCGCTGATGGGGGTGAACAACAACCGCGCGCGG	360
Qy	453	CCGCGGGGACCCCAATGCTCTCTGCAAGTGCACATGCAAAACGCTCTTGTTCAGAGCA	512
Db	361	CCGCGGGGACCCCAATGCTCTCTGCAAGTGCACATGCAAAACGCTCTTGTTCAGAGCA	420
Qy	513	TGAGATCACGAGAGTGGATTGTTTCAGATCATCATCTGTGTGTATGATGTTGA	572
Db	421	TGAGATCACGAGAGTGGATTGTTTCAGATCATCATCTGTGTGTATGATGTTGA	480
Qy	573	TGGTGTGTATCAACGTCCTGCGAGCAACCTAACCTGTCGACAGCTTCATCA	632
Db	481	TGGTGTGTATCAACGTCCTGCGAGCAACCTAACCTGTCGACAGCTTCATCA	540
Qy	633	GCCGCGACAGCCAGGGGCGAGAGAGAGAATGCCCCGTCTCTAGAAAGATGCTGTGGC	692
Db	541	GCCGCGACAGCCAGGGGCGAGAGAGAGAATGCCCCGTCTCTAGAAAGATGCTGTGGC	600
Qy	693	CCTCGGAGACACACATGTCACGGCCAAACGGAATCCCAAGACCGCAGGTCTAAGCCCCGCTC	752
Db	601	CCTCGGAGACACACATGTCACGGCCAAACGGAATCCCAAGACCGCAGGTCTAAGCCCCGCTC	660
Qy	753	GAGCCACAGCACCGCTGCGCGCTGCGCCCTTCGACCACAGGAGCGCTTCACACGCTTCC	812
Db	661	GAGCCACAGCACCGCTGCGCGCTGCGCCCTTCGACCACAGGAGCGCTTCCACACGCTTCC	720
Qy	813	AGCCACCTATTCGTAACCTGCGACACGAGATGACCTGCAACCAACATCTTCGCTGTAG	872
Db	721	AGCCACCTATTCGTAACCTGCGACACGAGATGACCTGCAACCAACATCTTCGCTGTAG	780
Qy	873	ACGGGGAAGAGCCCCACCTTACCAAGGGGCCCCGTGACCTCAGCTTGAGGACCCCGAGC	932
Db	781	ACGGGGAAGAGCCCCACCTTACCAAGGGGCCCCGTGACCTCAGCTTGAGGACCCCGAGC	840
Qy	933	AGCAGCTGAACTGAACCGGGAGTGCATGCGCGCACCCCAACAGAACATCTTCGACA	992
Db	841	AGCAGCTGAACTGAACCGGGAGTGCATGCGCGCACCCCAACAGAACATCTTCGACA	900
Qy	993	GTGACCTGATGATATGTGCGACAGGCTGGGCGGCTCTGCCCTCCGACGATTACTGGGCA	1053
Db	901	GTGACCTGATGATATGTGCGACAGGCTGGGCGGCTCTGCCCTCCGACGATTACTGGGCA	960
Qy	1053	TCAGGCGCACGTCGACAGGCGAGCGGCGGACATGAAGGGGCGCGCGCCACCTTACAGG	1112
Db	961	TCAGGCGCACGTCGACAGGCGAGCGGCGGACATGAAGGGGCGCGCGCCACCTTACAGG	1020
Qy	1113	AGGTCAATCGGCCACTACCGCGGGTCTCTCTTCAGCACACAGCAGAGATGGGCGGCTT	1172
Db	1021	AGGTCAATCGGCCACTACCGCGGGTCTCTCTTCAGCACACAGCAGAGATGGGCGGCTT	1080
Qy	1173	CCTTGCTGAGGGGACCCGGCTTCACACACACACATGCGCGCTCTTAAGAGCTGAGCCA	1233
Db	1081	CCTTGCTGAGGGGACCCGGCTTCACACACACACATGCGCGCTCTTAAGAGCTGAGCCA	1140
Qy	1233	TCTGAGCAAAAGAAAGATTAACAAGAAAGACACCTCTCTAAGGGTCCCCAGGGGGCC	1293
Db	1141	TCTGAGCAAAAGAAAGATTAACAAGAAAGACACCTCTCTAAGGGTCCCCAGGGGGCC	1200
Qy	1293	GGGCTGGGGCTCGTAGGTGAAGAGCGAG	1321
Db	1201	GGGCTGGGGCTCGTAGGTGAAGAAAGCGAG	1229

RESULT 11
ADW43368

RESULT 11

ADW43368

ID	ADM43368 standard; DNA; 4639 BP.
XX	
AC	ADM43368;
XX	
DT	24-MAR-2005 (first entry)
XX	
DE	Prostate cancer related gene, SEQ ID 166.
XX	
XX	Cytostatic; Gene Therapy; Prostate tumor; prostatic cancer; diagnosis;
KW	ds; gene.
XX	
OS	Homo sapiens.
XX	
PN	WO2004113571-A2.
XX	
PD	29-DEC-2004.
XX	
PF	25-JUN-2004; 2004WO-IB002394.
XX	
PR	26-JUN-2003; 2003US-0482595P.
XX	
PA	(EXON-); EXONHIT THERAPEUTICS SA.
XX	
PI	Einstein R, McGowan KM, Pando MP;
XX	
DR	WPI; 2005-057996/06.
XX	
PT	New isolated nucleic acid sequence that is expressed by human prostate
XX	cancer cells, useful as target for treating, preventing and/or diagnosing
PT	cancers, particularly prostate cancer.
XX	
PS	Claim 1; SEQ ID NO 166; 198bp; English.
XX	
XX	The present invention relates to novel nucleic acid sequences that are
CC	expressed by human prostate cancer cells. The nucleic acid sequences or
CC	the encoded proteins are useful as targets for treating, preventing
CC	and/or diagnosing cancers, particularly prostate cancer. The present
CC	sequence is one such nucleic acid of the invention.
XX	
SEQ	Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;

Query Match	93.0%	Score 1229	DB 14	Length 4839
Best Local Similarity	100.0%	Pred. No. 7.2e-184		
Matches 1229	Conservative	0	Mismatches	0
			Indels	0
			Gaps	0
QY	93	GGAAGCTAGCGGCGAGAGCTCAGCCCCCGGCGGCGAGCGCGCCCCGCTGCCAGCCATT	152	
Db	1	GGAAGCTAGGCGGCGAGAGCTCAGCCCCCGGCGGCGAGCGCGCCCCGCTGCCAGCCATT	60	
QY	153	TTCCGGATGCCAATCCCGCGGCGCATGCGCAACGCCCCCGGGGCTGCCGAGGGAGGCGCGGG	212	
Db	61	TTCCGGAGGCCAATCCCGCGGCGCATGCGCAACGCCCCCGGGGCTGCCGAGGGAGGCGCGGG	120	
QY	213	GAGCGCAGCGAGCGCGGCTCCCGCGCATGAGCCCGCGGCGCGCCCCGGAACTTGAGCGC	272	
Db	121	GAGCGCAGCGAGCGCGGCTCCCGCGCATGAGCCCCCGCGCGCCCCGGAACTTGAGCGC	180	
QY	273	GACCCGAGCCCGGCGAGGCGGAGGCGGCTTCCCGCGCGCGCTCTTGATGCGGGGC	332	
Db	181	GACCCGAGCCCGGCGAGGCGGAGGCGGCTTCCCGCGCGCGCTCTTGATGCGGGGC	240	
QY	333	CCCAACTCCGAGCG	392	
Db	241	CCCAACTCCGAGCG	300	
QY	393	GCGCGCGCGCGCGCGCTGCATGACGCGCTTGATGAGGAGTCAACAGACCGCGCGCGCG	452	
Db	301	GCGCGCGCGCGCGCGCTGCATGACGCGCTTGATGAGGAGTCAACAGACCGCGCGCGCG	360	
QY	453	CCGCGCGGAGCCCAATGTTCTCTGCAGGTGACACTGCAGAACGCTTTTGTTCAGAGGA	512	
Db	361	CCGCGCGGAGCCCAATGTTCTCTGCAGGTGACACTGCAGAACGCTTTTGTTCAGAGGA	420	

QY 773 GTGCGCCCTTGCGCCAGAGGAGCGCTTCCAGCGCTTCCAGCCACCTATCCGACTG 832
 DB 361 GTGCGCCCTTGCGCCAGAGGAGCGCTTCCAGCGCTTCCAGCCACCTATCCGACTG 420
 QY 833 CAGCAGAGATGACCTGCAACCCACCACTTCTGCTGTGAGACGGGAGAGCCCCCAACC 892
 DB 421 CAGCAGAGATGACCTGCAACCCACCACTTCTGCTGTGAGACGGGAGAGCCCCCAACC 480
 QY 893 TACCAAGGCGCCCTGCAACCTTCCAGTGTGGAGACCCCGAGCAGACTGGAATGAACCGG 952
 DB 481 TACCAAGGCGCCCTGCAACCTTCCAGTGTGGAGACCCCGAGCAGACTGGAATGAACCGG 540
 QY 953 GAGTGGTGGCGGACCCCAAGAAAGAAACATCTTCCAGAGTGAACCTGATGATGATGATG 1012
 DB 541 GAGTGGTGGCGGACCCCAAGAAAGAAACATCTTCCAGAGTGAACCTGATGATGATGATG 600
 QY 1013 AGGCTGGGCGGCGCCCTGCGCCCGCCAGAGTAAGTGGGATCAGCCGCACTGATACGGC 1072
 DB 601 AGGCTGGGCGGCGCCCTGCGCCCGCCAGAGTAAGTGGGATCAGCCGCACTGATACGGC 660
 QY 1073 AGCGGCGGCGGATGAGAGGCGCGCGCCGACCTTACAGAGAGTATGAGCCACTACCGG 1132
 DB 661 AGCGGCGGCGGATGAGAGGCGCGCGCCGACCTTACAGAGTATGAGCCACTACCGG 720
 QY 1133 GGGTCTCTCTTCCAGACACGAGCAGAGAGTGGGCGCGCCCTCTGCTGAGAGGCGACCGCG 1192
 DB 721 GGGTCTCTCTTCCAGACACGAGCAGAGAGTGGGCGCGCCCTCTGCTGAGAGGCGACCGCG 780
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 DB 781 CTCACACACACACATCGCGCCCTTACAGAGCGAGCATCTGAGAGAAAGAGAGAT 840
 QY 1253 AAACGAAAGACACCTCTCTAG 1276
 DB 841 AAACGAAAGACACCTCTCTAG 864

RESULT 15

AAA75151
 ID AAA75151 standard; CDNA; 969 BP.

AC AAA75151;

DT 15-JAN-2001 (first entry)

DE CDNA encoding a human TANGO 261 polypeptide.

XX TANGO 266; TANGO 216; TANGO 261; TANGO 262; TANGO 267;
 KW cellular proliferation; cellular differentiation; cellular adhesion;
 KW von Willebrand factor-associated disorder; cell trafficking; cancer;
 KW hematopoietic associated disease; atelectasis; pulmonary congestion;
 KW edema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
 KW intestinal disorder; spleen associated disease; renal disorder;
 KW cardiovascular disorder; ischemic heart disease; hydrocephalus;
 KW brain herniation; iatrogenic disease; inflammation; meningitis;
 KW Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease;
 KW Multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.

OS Homo sapiens.

PH Key Location/Qualifiers

FT CDS 6..764 /tag= a /product= "TANGO 261"

FT sig_peptide 6..89 /tag= b

FT mat_peptide 90..764 /tag= c

PN WO200052022-A1.

XX 08-SEP-2000.

XX

PF 01-MAR-2000; 2000WO-US005226.
 XX 01-MAR-1999; 99US-0122458P.
 PR (MILL-) MILLENNIUM PHARM INC.
 PA Barnes TM, Holtzman DA, Sharp JD, Fraser CJ,
 PI WPI; 2000-579269/54.
 DR P-PSDS; AAB18449.
 XX Novel human and murine secreted proteins designated TANGO 216, 261, 262,
 PT 266 and 267 useful as modulating agents of cellular processes, e.g. for
 PT treating cancer.
 PS Claim 2; Fig 5; 175pp; English.

XX The present sequence encodes a human TANGO 261 polypeptide. The
 CC specification also describes TANGO 266, TANGO 216, TANGO 262, and TANGO
 CC 267. The TANGO polypeptides can be used to modulate cellular
 CC proliferation, modulate cellular differentiation and/or modulate cellular
 CC adhesion. The proteins can be used to treat any von Willebrand factor-
 CC associated disorder, regulate extracellular matrix structuring, cellular
 CC adhesion, and cell trafficking and/or migration, modulate cellular
 CC interactions, modulate cell adhesion in proliferative disorders, such as
 CC cancer, modulate the proliferation, differentiation, and/or function of
 CC cells that appear in the bone marrow, and leukocytes, treat bone marrow,
 CC blood and hematopoietic associated diseases and disorders, atelectasis,
 CC pulmonary congestion or edema, emphysema, chronic bronchitis, bronchial
 CC asthma and bronchiectasis, intestinal disorders, spleen associated
 CC diseases, modulate renal disorders, treat cardiovascular disorders such
 CC as ischemic heart disease, modulate the proliferation, differentiation,
 CC and/or function of bone and cartilage cells and to treat bone and/or
 CC cartilage associated diseases or disorder. They may also be used to treat
 CC disorders associated with the ovaries, cerebral edema, hydrocephalus,
 CC brain herniations, iatrogenic disease, inflammations, bacterial and viral
 CC meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's
 CC disease, multiple sclerosis, brain cancers, hydrocephalus and
 CC encephalitis, and treat hepatic disorders

XX Sequence 969 BP; 211 A; 316 C; 294 G; 148 T; 0 U; 0 Other;

Query Match 60.8%; Score 803.2; DB 3; Length 969;
 Best Local Similarity 99.6%; Pred. No. 4.3e-117;
 Matches 805; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 514 GAGATCAACGAGGCTGAGGTTGTTCAATCATCATCATGCTGTGTGATGATGAT 573
 DB 2 GAGATGAGCGAGGCTGAGGTTGTTCAATCATCATCATGCTGTGTGATGATGAT 61
 QY 574 GGTGTGTGATCACTGCTGCTGAGCCACTAAGCTGTCTGACAGGCTTCTCATAG 633
 DB 62 GGTGTGTGATCACTGCTGCTGAGCCACTAAGCTGTCTGACAGGCTTCTCATAG 121
 QY 634 CCGGACAGCCAGGGGCGAGAGAGAAAGTCCCTGCTCTCAGAAAGATGCTGTGGCC 693
 DB 122 CCGGACAGCCAGGGGCGAGAGAGAAAGTCCCTGCTCTCAGAAAGATGCTGTGGCC 181
 QY 694 CTGAGAGACACAGTGTACGCAACGAAATCCAGAGCCGAGGTTACGCGCCGCTCG 753
 DB 182 CTGAGAGAGACACAGTGTACGCAACGAAATCCAGAGCCGAGGTTACGCGCCGCTCG 241
 QY 754 GCCCAACGACCGCTGCGCGCTGCGCCCTTGGCCAGCGGAGAGGCTTCCACCGCTTCCA 813
 DB 242 GCCCAACGACCGCTGCGCGCTGCGCGCCCTTGGCCAGCGGAGAGGCTTCCACCGCTTCCA 301
 QY 814 GCCCAACGACCGCTGCGCGAGCAGAGATGACCTGCAACCACTCTGCTGTGAGA 873
 DB 302 GCCCAACGACCGCTGCGCGAGCAGAGATGACCTGCAACCACTCTGCTGTGAGA 361
 QY 874 CCGGAGAGAGCCCGACCTTACAGAGGCGCTTGCACCTTCAGGTTGGGAGCCCGAGCA 933
 DB 362 CCGGAGAGAGCCCGACCTTACAGAGGCGCTTGCACCTTCAGGTTGGGAGCCCGAGCA 421


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OY 934 GAGCTGGAACCTGAACCGGGAGTCGGTGGCCGACACCCCAACAGAACCATTTGACAG 993
DB |||||
DB 422 GAGCTGGAACCTGAACCGGGAGTCGGTGGCCGACACCCCAACAGAACCATTTGACAG 481
OY 994 TGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1053
DB |||||
DB 482 TGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 541
OY 1054 CAGCGCCACGTCCTACGCGAGCGCGCGCGCATGGAAGGGCCGCGCCGACCTACAGCGA 1113
DB |||||
DB 542 CAGCGCCACGTCCTACGCGAGCGCGCGCGCATGGAAGGGCCGCGCCGACCTACAGCGA 601
OY 1114 GGTTCATCGGCCACTACCGCGGGTCTCTCTTCCAGCACACGACAGAGAGTGGGCGGCTTC 1173
DB |||||
DB 602 GGTTCATCGGCCACTACCGCGGGTCTCTCTTCCAGCACACGACAGAGAGTGGGCGGCTTC 661
OY 1174 CTTGCTGAGGGGAGCCCGGCTCCACACACACATCGGCGCCCTAGAGAGGCGAGCCAT 1233
DB |||||
DB 662 CTTGCTGAGGGGAGCCCGGCTCCACACACACATCGGCGCCCTAGAGAGGCGAGCCAT 721
OY 1234 CTGAGCAAGAGAGAGATTAACAGAAAGGACACCTCTCTAGGGTCCCAGGGGGCCG 1293
DB |||||
DB 722 CTGAGCAAGAGAGAGATTAACAGAAAGGACACCTCTCTAGGGTCCCAGGGGGCCG 781
OY 1294 GGTGAGGGCTGCTAGGTGTAAGGACAG 1321
DB |||||
DB 782 GGTGAGGGCTGCTAGGTGTAAGGACAG 809
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Job time : 903.636 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 28, 2006, 09:05:04 ; Search time 6116.44 Seconds
(without alignments)
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Title: US-09-934-249-1

Perfect score: 1321

Sequence: 1 cgaccgcggtctcgagcga.....ctgcgtcagtcgaaagcag 1321

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 2339354128 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2: *
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4: gb_hic: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_est7: *
9: gb_g881: *
10: gb_g882: *
11: gb_g883: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	858.8	65.0	1038	1	AL517150 AL517150
C 3	766.8	58.0	967	5	BQ641849 AGENCOURT
C 4	766.8	58.0	1046	3	BM922276 AGENCOURT
C 5	764.2	57.9	1059	1	AL543170 AL543170
C 6	741.1	56.1	901	4	CR612083 full-1eng
C 7	736.4	55.6	916	5	BQ954555 AGENCOURT
C 8	734.2	55.6	850	1	AL558881 AL558881
C 9	734.2	55.6	850	5	BX362396 BX362396
C 10	714.6	54.1	867	5	AL558882 AL558882
C 11	691.2	52.3	945	1	BUS39219 AGENCOURT
C 12	686.6	52.0	850	5	BU602918 AGENCOURT
C 13	651	49.3	780	10	AY419334 AY419334
C 14	637.4	48.3	647	8	DN992322 TC124411
C 15	634.2	48.0	711	7	CJ028468 CJ028468
C 16	630.6	47.7	1207	4	AK008976 AK008976
C 17	614.6	46.5	782	3	BQ015170 UI-H-BD1
C 18	607.4	46.0	609	5	BQ636742 hbl3h06.Y
C 19	591.4	44.8	601	8	DN991959 TC113206
C 20	588.8	44.6	605	7	CV028567 CV028567
C 21	578.4	43.8	890	5	BQ690750 AGENCOURT
C 22	570.4	43.2	973	5	BU169156 AGENCOURT

C 23	568.8	43.1	572	5	BX641317 BX641317
C 24	567.4	43.0	729	5	BQ575741 BQ575741
C 25	564.8	42.8	730	5	BM677602 UI-B-E01-
C 26	563.2	42.6	728	5	BU683523 UI-CF-E01
C 27	550	41.6	551	3	BM141979 BM141979
C 28	545	41.3	553	8	DN990606 DN990606
C 29	529.8	40.1	894	3	BI851941 BI851941
C 30	521	39.4	1068	5	BUS27705 BUS27705
C 31	507	38.4	780	10	AY419335 AY419335
C 32	501.6	38.0	588	3	BM483503 BM483503
C 33	493.6	37.4	693	1	AT761441 AT761441
C 34	493.4	37.4	655	5	BQ691705 BQ691705
C 35	487.6	36.9	646	10	CG784226 CG784226
C 36	486	36.8	1400	5	BM559329 BM559329
C 37	480.8	36.4	964	5	BUS59860 BUS59860
C 38	477.6	36.2	646	5	BU859841 BU859841
C 39	476.4	36.1	651	6	CB554226 CB554226
C 40	475.2	36.0	624	10	AY419336 AY419336
C 41	468.8	35.5	1280	5	BQ691500 BQ691500
C 42	468	35.4	857	2	BG323347 BG323347
C 43	468	35.4	974	2	BB624904 BB624904
C 44	465.8	35.3	744	5	BU414421 BU414421
C 45	461	34.9	763	3	BI646175 BI646175

ALIGNMENTS

RESULT 1
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LOCUS AL578575 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
DEFINITION CDNA clone CSODK001YC24 3-PRIME, mRNA sequence.

ACCESSION AL578575 GI:46257448
VERSION AL578575.3
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1005)
AUTHORS Li W.B., Gruber C., Jessee J. and Polayes D.
TITLES Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 16, 2001 this sequence version replaced gi:31316780.

Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 9945.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdnas=CSODK001B12NP1ec=9945.r.
Location/Qualifiers

FEATURES

source
1..1005
/organism="Homo sapiens"
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/clone="CSODK001YC24"
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/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

QY 818 ACCTATCGCTACCTGACAGAGATGACCTGACACCCACCATCTGCTGACAGCGG 877
 DB 620 ACCTATCGCTACCTGACAGAGATGACCTGACACCCACCATCTGCTGACAGCGG 561
 QY 878 GAGGAGCCCGGACCTTACAGAGGCGGCTGACACCTTCCAGCTTGGGAGCCCGGAGAGCG 937
 DB 560 GAGGAGCCCGGACCTTACAGAGGCGGCTGACACCTTCCAGCTTGGGAGCCCGGAGAGCG 501
 QY 938 CTGGAATGAACTGGAGAGTGGTGGGCGGACCCCGGAGAGAGAGAGAGAGAGAGAGAG 997
 DB 500 CTGGAATGAACTGGAGAGTGGTGGGCGGACCCCGGAGAGAGAGAGAGAGAGAGAGAG 441
 QY 998 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1057
 DB 440 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 381
 QY 1058 GCCACGCTGCTACGAGCGGCGGCGGCGATGAGAGGCGGCGGCGGCGGCGGCGGCGGCG 1117
 DB 380 GCCACGCTGCTACGAGCGGCGGCGGCGATGAGAGGCGGCGGCGGCGGCGGCGGCGGCG 321
 QY 1118 ATCGGCTGCTACGAGCGGCGGCGGCGATGAGAGGCGGCGGCGGCGGCGGCGGCGGCG 1177
 DB 320 ATCGGCTGCTACGAGCGGCGGCGGCGATGAGAGGCGGCGGCGGCGGCGGCGGCGGCG 261
 QY 1178 CTGAGAGGAG 1237
 DB 260 CTGAGAGGAG 201
 QY 1238 AGCAAG 1297
 DB 200 AGCAAG 141
 QY 1298 GGGGCTGCTGAGTGAAG 1321
 DB 140 GGGGCTGCTGAGTGAAG 117

RESULT 3
 LOCUS B0641849 967 bp mRNA linear EST 15-JUL-2002
 DEFINITION AGENCOURT 8287174 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:6292265
 5', mRNA sequence.
 ACCESSION B0641849
 VERSION B0641849.1 GI:21766021
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini;
 Homiidae; Homo.
 REFERENCE 1 (bases 1 to 967)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLCM2493 row: 9 column: 18
 High quality sequence stop: 571.
 Location/Qualifiers
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 /mol_type="mRNA"
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/clone_id="NIH_MGC_43"
 /note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:
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 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library. |"
 ORIGIN
 Query Match 58.0%; Score 766.8; DB 5; Length 967;
 Best Local Similarity 99.1%; Pred. No. 1.5e-12;
 Matches 771; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 524 GAGCTGAGATTGTTTCATATCATCATCTGTTGTTGATGATGATGATGATGATGATGATG 583
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 QY 584 ATCAAGTGCCTGAGGACCTACAGAGCTGTCAGAGGCTCTTCATCAGCGGACAGC 643
 DB 61 ATCAAGTGCCTGAGGACCTACAGAGCTGTCAGAGGCTCTTCATCAGCGGACAGC 120
 QY 644 CAGGGCGGAGAGAGAGATGCTCTCTCAGAGAGATGCTGAGGCTCTGAGAGC 703
 DB 121 CAGGGCGGAGAGAGAGATGCTCTCTCAGAGAGATGCTGAGGCTCTGAGAGC 180
 QY 704 ACAGTGCAAGCAAGCAATCCAGAGCGGAGCTCTACGCGGCTCTGAGAGC 763
 DB 181 ACAGTGCAAGCAAGCAATCCAGAGCGGAGCTCTACGCGGCTCTGAGAGC 240
 QY 764 GCGCTGCGGCTGCGGCTCTGCGGCGGAGGAGGCTCTCAAGGCTCTCAAGGCTCTAT 823
 DB 241 GCGCTGCGGCTGCGGCTCTGCGGCGGAGGAGGCTCTCAAGGCTCTCAAGGCTCTAT 300
 QY 824 CCGTACCTGACAGAGAGATGACCTGACAGGAGGAGGCTCTGAGAGGAGAGAG 883
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 QY 944 CTGAACCGGAGATGCTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1003
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 QY 1004 GATAGTGCAGAGCTGAGGCGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1063
 DB 481 GATAGTGCAGAGCTGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
 QY 1064 TGCTACGAGAGCGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1123
 DB 541 TGCTACGAGAGCGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
 QY 1124 CACTACCGGAGTCTCTCTTCCAGAGACAGAGAGAGGAGGAGGAGGAGGAGGAGGAG 1183
 DB 601 CACTACCGGAGTCTCTCTTCCAGAGACAGAGAGAGGAGGAGGAGGAGGAGGAGGAG 660
 QY 1184 GGGAGCGGCTCACACACACACATCGGCGGCTTAGAGAGGAGGAGGAGGAGGAGGAG 1243
 DB 661 GGGAGCGGCTCACACACACACATCGGCGGCTTAGAGAGGAGGAGGAGGAGGAGGAG 720
 QY 1244 GAGAGGATTAACAGAAAGAGACCTCTCTAGAGGCTCCAGAGGAGGAGGAGGAGGAG 1301
 DB 721 GAGAGGATTAACAGAAAGAGACCTCTCTAGAGGCTCCAGAGGAGGAGGAGGAGGAG 778

RESULT 4
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 DEFINITION AGENCOURT 6707077 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:574437
 5', mRNA sequence.

ACCESSION	BM922276
VERSION	BM922276.1
KEYWORDS	GI:19372655
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Mammalia; Euarchontoglires; Primates; Catarrhini;
JOURNAL	Hominidae; Homo.
COMMENT	1 (bases 1 to 1046) NIH-MGC http://mgc.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strusberg, Ph.D. Email: cgabbs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLNL12791 row: n column: 06 High quality sequence stop: 671. location/Qualifiers 1..1046
FEATURES	
SOURCE	

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/note="Organ: site 1: Notti; site 2: Ectov; Vector:
pcwv-SpOTr; Site 1: Notti; site 2: Ectov (destroyed); RNA
source anonymous_pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dt primed and directionally cloned (Ectov site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC library."

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ORIGIN

Query Match	58.0%;	Score 766;	DB 3;	Length 1046;
Best Local Similarity	95.8%;	Pred. No. 2.1e-132;		
Matches 818; Conservative	0;	Mismatches 32;	Indels 4;	Gaps 3;

QY	347	CCGCGGCGGAGACCC	CCCCCGCGCGCGCC	CCGAGGCCCCCGCGGCC	CCCGCGCGCGCGCGCGCG	406
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QY	407	CCGTCATATGACCG	CGCTTGATGGGGGT	CAACAGCACCGCGCGCGCGCGCGCGGACGCC		466
Db	61	CCGTCAATGACACCG	CTTGATGGGGGT	CAACAGCACCGCGCGCGCGCGCGCGGACGCC		120
QY	467	AATGTCTCTGCACG	TGCATGCAACCGCTCTT	TTGTTCAAGAGATGGAGATCA	CGAG	526
Db	121	AATGTCTCTGCACG	TGCATGCAACCGCTCTT	TTGTTCAAGAGATGGAGATCA	CGAG	180
QY	527	CTGGAGTTTGTCAG	ATCATCATCATCGTGGTGGT	GATGATGATGATGATGATG		586
Db	181	CTGGAGTTTGTCAG	ATCATCATCATCGTGGTGGT	GATGATGATGATGATGATG		240
QY	587	ACGTGCTCTGAGG	CACTAACAGCTGTGCA	CGSTCTTTATCAGCCGGACA	CGCCAG	646
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QY	647	GGCGCGAGAGAGAA	GATGCTGTCTCAAGAA	GATGCTGTGGGCCCTCTCGAGAGACAA		706
Db	301	GGCGCGAGAGAGAA	GATGCTGTCTCAAGAA	GATGCTGTGGGCCCTCTCGAGAGACAA		360
QY	707	GTGTCAAGGAAGGA	ATCCAGACCGGACAG	GTCTAAGCCCGCTCGGCCCA	CCGACGCG	766

Db	361	GTGTCAGAGCAACGGAAATCCACAGAGCCGACAGTCAACGCCCGCTCGAGCCACGACGAC	420
Oy	767	CTGGCCCGTGGCCGCCCTTGGCCGACGGGAGCGCTTCCACCGCTTTCAGGCCACCTATCCG	826
Db	421	CTGGCCCGTGGCCGCCCTTGGCCGACGGGAGCGCTTCCACCGCTTTCAGGCCACCTATCCG	480
Oy	827	TACCTGACGACGAGATGCACCTGCAACCCACCATCTCGCTGTGACGCGGAGAGAGCCC	886
Db	481	TACCTGACGACGAGATGCACCTGCGCCGCCACCATCTCGCTGTGACGCGGAGAGAGACC	540
Oy	887	CCACCTTACCAAGGGCCCCCTGCAACCTTCAGCTTGGGAGCCCGGACGACAGCTGGAACTG	946
Db	541	CCACCTTACCAAGGGCCCCCTGCAACCTTCAGCTTGGGAGCCCGGACGACAGCTGGAACTG	600
Oy	947	AACCGGAGTGGGTGCGCGCACCCCAACGAAACATCTTCGACAGTGAACCTGATGAT	1006
Db	601	AACCGGAGTGGGTGCGCGCACCCCAACGAAACATCTTCGACAGTGAACCTGATGAT	660
Oy	1007	AGTGCAGAGCTGGGCGGCGCCCTTGCCGCCCCCGACAGCTAACTCGGGCATCAGCGCACGTGC	1066
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Oy	1067	TACGGCAGCGGCGG-GCGCATGAGAGGGACGCGC-CCACACTTACAGCGAGGTCAATCGACC	1124
Db	721	TACGGCAGCGGCGGCGCGCATGAGAGGGCGCGGCCCCACCTAACGAGGAAGTCAATCGGCC	780
Oy	1125	ACTA-CCCGGGGTCTCTTTCGAGCACACGACGACAGCAGTGGCGCGCTCTTCTTGCTGGA	1182
Db	781	ACTAACCCTGGGGGTCTCTTTCGAGCACACCANCATATCAACTGGGGCGCGCTCTTCTTGCC	840
Oy	1183	GAGGACCCGCGCTCC 1196	
Db	841	CTGGAGAGGGAAAC 854	

RESULT 5	AL543170	1059 bp	mRNA	linear	EST 24-MAR-2004
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DEFINITION	AL543170 Homo sapiens PLAGENRA COT 25-NORMALIZED Homo sapiens cDNA clone CS001002Y103 5-PRIME, mRNA sequence.				
ACCESSION	AL543170				
VERSION	AL543170.3	GI:45718734			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Mammalia; Eumetazoa; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 1059)				
AUTHORS	Li, W.B., Gruber, C., Jesssee, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished (2001)				
COMMENT	On Feb 15, 2001 this sequence version replaced gi:31265017.				

FEATURES	location/Qualifiers
source	1. .1059

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ORIGIN

/note="1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

Query Match 57.9%; Score 764.2; DB 1; Length 1059;
Best Local Similarity 91.1%; Pred. No. 4,5e-132;
Matches 866; Conservative 20; Mismatches 54; Indels 11; Gaps 7;

102 GCGGAGAGGCTCACCCCGGCGAGCGCGCCCTGCGCAGCCCATTTTCGGAGC 161
1 GCGGAGAGGCTCACCCCGGCGAGCGCGCCCTGCGCAGCCCATTTTCGGAGC 60
162 CCACCCGCGGCGACTGCGGAGCGCCCGGCGCTGCGGAGGAGCGCGGCGCGCAGC 221
61 CCACCCGCGGCGACTGCGGAGCGCCCGGCGCTGCGGAGGAGCGCGGCGCGCAGC 120
222 GAGGCGCGCTCCCGGCGACTGAGCCCGCGCGCCCGGGAATTGGGCGCGAGCCGAGC 281
121 GACGCGCGCTCCCGGCGACTGAGCCCGCGCGCCCGGGAATTGGGCGCGAGCCGAGC 180
282 CCGGCGAGCGCGGCGCGCTCCCGCGCGCGCGCC-TCCTGCAATGCGGCGCGCGAGCTC 340
181 CCGGCGAGCGCGGCGCGCTCCCGCGCGCGCGCCGCGCTGCTGCAATGCGGCGCGAGCTC 240
341 CCGGCGCGCGGCGGAGC 400
241 CCGGCGCGCGGCGGAGC 300
401 GCGGCGCGCTCCATGACCGCTTGTATGAGGAGGCTCAACAGACCGCGCGCGCGCGCGCG 460
301 GCTTACCTTTTCATGACCGCTTGTATGAGGAGGCTCAACAGACCGCGCGCGCGCGCTTC 360
461 GAGCCCAATGTCCTCGAC--GTGCACTGCAAAAGCTCTTGTTCAGACATGAGA 518
361 WACCCCAATTTCTTCTTCACTTGTCTCATTTCAACACTTTTTCATTAACATGAGA 420
519 TCACGAGCTGAGATTGTTGATCATCATCATGCTGCTGATGATGATGATGATGATG 578
421 TCACGAGCTGAGATTGTTGATCATCATCATGCTGCTGATGATGATGATGATGATG 480
579 TGGTATCATCGTCTGCTGAGCCACTACAGTGTCTGCAAGGCTCTTCATCAGCGCGC 638
481 TGGTATCATCGTCTGCTGAGCCACTACAGTGTCTGCAAGGCTCTTCATCAGCGCGC 540
639 ACACGCGAGGCGGAGAGAGAGATGCTGCTGCTGCAAGAGATGCTGCGCGCTGCG 698
541 ACACGCGAGGCGGAGAGAGAGATGCTGCTGCTGCAAGAGATGCTGCGCGCTGCG 600
699 AGAGCAGATGTCAGGCAACGAGATCCAGAGCGGAGCTTACGCCCGCTCGGCGCA 758
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759 CCGACCGCTGCGCTGCGCGCTTGTGCGCAAGGCGGAGCTTTCACCGCTTCAGCCCA 818
661 CCGACCGCTGCGCTGCGCGCTTGTGCGCAAGGCGGAGCTTTCACCGCTTCAGCCCA 720
819 CCGATCCGATCCGAGAGAGATGAGCTGCAACCAATCTGCTGCTGAGAGCGGAG 878
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781 AGAG--CGCGCGCGCGCGCGCGCTTTCAGGAGCTTCGAGAGCGGAGCAGC 837
939 TGGATCTGAACCGGAGGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 998
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896 TGGATCTGAACCGGAGGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 943

RESULT 6
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DEFINITION
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VERSION
KEYWORDS
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AUTHORS
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JOURNAL
REMARK
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Full-length cDNA clone CSDBJ015YR12 of T cells (Jurkat cell line)
Cot 10-normalized of Homo sapiens (human).
CR612083
CR612083.1 GI:50492890
HTC; CDS; CDS; CDS
SOURCE
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo
1 (bases 1 to 901)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Parade Avenue
2 (bases 1 to 901)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage;
BP 191 91006 Evry cedex - FRANCE (E-mail: sequef@genoscope.cns.fr)
- Web: www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen
Location/Qualifiers
1. 901
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Best Local Similarity 100.0%; Pred. No. 9.5e-128;
Matches 741; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 GTGATCAGTGTCTGCTGAGCCACTACAGTGTCTGCAAGGCTCTTCATCAGCGCGC 60
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Db AGCCAGGCGGCGGAGAGAGATGCTGCTCTGCAAGAGATGCTGCGCGCTGCGAG 120
61 AGCCAGGCGGCGGAGAGAGATGCTGCTCTGCAAGAGATGCTGCGCGCTGCGAG 760
701 AGCAAGTGTACGAGCAAGGAATCCAGAGCGCGAGCTTACGCCCGCTGCGCGCAC 760
121 AGCAAGTGTACGAGCAAGGAATCCAGAGCGCGAGCTTACGCCCGCTGCGCGCAC 180
761 GACCGCTGCGCGCTGCGCGCTTGTGCGCGAGCGGAGCGCTTACCGCTTCAGCGCAC 820
181 GACCGCTGCGCGCTGCGCGCTTGTGCGCGAGCGGAGCGCTTACCGCTTCAGCGCAC 240
821 TATCCGTAACCTGACAGAGAGATGAGCTGCGCGCACCATCATCTGCTGCAAGCGGAG 880
241 TATCCGTAACCTGACAGAGAGATGAGCTGCGCGCACCATCATCTGCTGCAAGCGGAG 300
881 GAGCGCGCGCGCTTACAGGCGCGCGCTGCAACCTTCAGCTTTCGAGAGCGGAGCG 940
301 GAGCGCGCGCGCTTACAGGCGCGCGCTGCAACCTTCAGCTTTCGAGAGCGGAGCG 360
941 GAACTGAACCGGAGAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1000

Db 361 GAACTGAACCGGAGTCCGTGCGGACACCCCAACAGACCATTTTGACAGTACTG 420
Qy 1001 ATGATAGTCCAGGCTGAGCGGCCCCCTGCCCCCAGACAGTACTCGGACATCGGCC 1060
Db 421 ATGATAGTCCAGGCTGAGCGGCCCCCTGCCCCCAGACAGTACTCGGACATCGGCC 480
Qy 1061 ACGTCTACGCGAGCGGCGGCGCATGAGAGGCGCGCCCACTTAAGAGAGTCAATC 1120
Db 481 ACGTCTACGCGAGCGGCGGCGCATGAGAGGCGCGCCCACTTAAGAGAGTCAATC 540
Qy 1121 GCGCACTACCGGAGGCTCTCTCTTCCAGACACGACAGAGTGGCGCCCTCTTGTG 1180
Db 541 GCGCACTACCGGAGGCTCTCTCTTCCAGACACGACAGAGTGGCGCCCTCTTGTG 600
Qy 1181 GAGGGAGCCCGGCTCCACCAACACATCGCGCCCTTGAAGAGCGCATCTGAGC 1240
Db 601 GAGGGAGCCCGGCTCCACCAACACATCGCGCCCTTGAAGAGCGCATCTGAGC 660
Qy 1241 AAAGAAAGATTAACAGAAAGACACCTCTCTTGGGTCCCAAGGGGGCGGGCTGG 1300
Db 661 AAAGAAAGATTAACAGAAAGACACCTCTCTTGGGTCCCAAGGGGGCGGGCTGG 720
Qy 1301 GCTGCTAGGTGAAGGAG 1321
Db 721 GCTGCTAGGTGAAGGAG 741

RESULT 7
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LOCUS B0954555
DEFINITION IMAGE:6204609 5', mRNA sequence.

ACCESSION B0954555
VERSION B0954555.1 GI:22370033
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 916)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaab-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Plate: L1AM13626 row: C column: 10
High quality sequence stop: 669.
Location/Qualifiers

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Directionally cloned using the following adaptors:
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5'-GACTAGTCTACATCGGCGGCGCCCT(15)-3'. Site selected >
1 kb for average insert length 1.87 kb. This is a primary

library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."

ORIGIN
Query Match 55.7%; Score 736.4; DB 5; Length 916;
Best Local Similarity 95.7%; Pred. No. 6.8e-127;
Matches 800; Conservative 0; Mismatches 31; Indels 5; Gaps 4;

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Db 1 GCGCGGCGGAGGCCCCCGCGCGCCCGAGCCCCCGCGCGCGCGCGCGCGCC 60
Qy 404 GCGCGGCGGAGGCCCCCGCGCGCCCGAGCCCCCGCGCGCGCGCGCGCGCC 463
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Qy 464 CCCAATGCTCTCTCAGTGAACCTGCAAAAGCTTTGTTCCAGACATGAGATACG 523
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Qy 524 GAGCTGAGATTGTTCAATCATCATCATCATCATCATCATCATCATCATCATCAT 583
Db 181 GAGCTGAGATTGTTCAATCATCATCATCATCATCATCATCATCATCATCATCAT 240
Qy 584 ATCACTGCTCTCTGAGCTCACTCACTCACTCACTCACTCACTCACTCACTCACT 643
Db 241 ATCACTGCTCTCTGAGCTCACTCACTCACTCACTCACTCACTCACTCACTCACT 300
Qy 644 CAGGGCGGAGAGAGAGAGATGCTGCTCAGAGAGATGCTGAGGCTCTGAGAGC 703
Db 301 CAGGGCGGAGAGAGAGAGATGCTGCTCAGAGAGATGCTGAGGCTCTGAGAGC 360
Qy 704 ACAGTGTACGAGCAACGAAATCCAGAGCGGAGCTTACGCGCTCGAGCCACGAC 763
Db 361 ACAGTGTACGAGCAACGAAATCCAGAGCGGAGCTTACGCGCTCGAGCCACGAC 420
Qy 764 GCGCTGCGCGTCCCGCCCTTCCAGAGGAGGCTTCCAGCGCTTCAGGCCACGAT 823
Db 421 GCGCTGCGCGTCCCGCCCTTCCAGAGGAGGCTTCCAGCGCTTCAGGCCACGAT 480
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Db 541 CCCCACCTTACAGAGGCGCTTGCACCTTCCAGCTTGGAGAGCCCGAGACAGCTGGA 600
Qy 944 CTGAACCGGAGTGGTGGCGGACCCCAAGAACCAATCTTGCAGAGTCACTGATG 1003
Db 601 CTGAACCGGAGTGGTGGCGGACCCCAAGAACCAATCTTGCAGAGTCACTGATG 660
Qy 1004 GATAGTGC-AGGCTGGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1061
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DEFINITION Homo sapiens cDNA clone CS0D015VF12 3-PRIME, mRNA sequence.
ACCESSION AL558881

VERSION AL58881.3 GI:46184268
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo
 1 (bases 1 to 850)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On Feb 15, 2001 this sequence version replaced gi:31283014.
 CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 9945.x
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?c=CS0D015DC06NP1&c=9945.x
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 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized."
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 Query Match 55.6%; Score 734.2; DB 1; Length 850;
 Best Local Similarity 99.3%; Pred. No. 1.8e-126;
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 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 867)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 5, 2003 this sequence version replaced gi:30378625.
 CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and EcoR V
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 9945.x
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?c=CS0D014CG08NP1&c=9945.x
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 /note="1st strand cDNA was primed with a NotI-oligo (dT)
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 was normalized."
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 Query Match 54.1%; Score 715; DB 5; Length 867;
 Best Local Similarity 96.2%; Pred. No. 6.5e-123;
 Matches 731; Conservative 16; Mismatches 11; Indels 2; Gaps 2;

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OY		622	GTCCTTCAATCACCGGCCACAGCCCAAGGGCGAGAGAGAAGATGCTCTGTCTCGAANAAG	681
Db		807	GTCCTTATCATGACCSBGACACAGCGGGCGGAGGAGAGMAATGCGCTTKTYTCAGAAAG	748
OY		682	ATGECTGTGGCCCTCTCGAGAGACACAGTGTCAAGGCAACGGAAATCCCAAGCCGCAAGTCTA	741
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Db		628	CCACCGCTTCAGCCCACTTATCCGTACNTGNAGNAAGATMGACNTGCGGCCACCAT	569
OY		862	CTCGCTGTCAACGGGGAGAGAGCCCCCAACCTTACAGAGGCCCTGTGCAACCTTCAGCTTG	921
Db		568	CTCGCTGTCAACGGGGAGAGAGCCCCCAACCTTACAGAGGCCCTGTGCAACCTTMAgTTTCG	509
OY		922	GGACCCCGAGGCGAGCTGGAACTGAACCGGGAGTCCGGTGGCGGCAACCCCAAAGAAAC	981
Db		508	GGACCCCGAGMAAGAGCTGGAACTGAACCGGGAGTCCGGTGGCGGCAACCCCAAAGAAAC	449
OY		982	CATCTTCGACAGTGAACCTGATGATATGTGCAGGCTGGGCGGGCCCTGTCCCCTCCAGCAG	1041
Db		448	CATCTTCGACAGTGAACCTGATGATATGTGCAGGCTGGGCGGGCCCTGTCCCCTCCAGCAG	389
OY		1042	TAACTTCGGGCAATCAGCGCCACGTGCTTACGSCAGCGCGGCGCATATGAGGGGCGCGCGC	1101
Db		388	TAACTTCGGGCAATCAGCGCCACCTGTCTTACGSCAGCGCGGCGCGCATATGAGGGGCGCGCGC	329
OY		1102	CACCTTACAGGAGGTCATTCGGGCACTAACCCGGGGTCTCTTTCAGGACCAAGCAGAGCAG	1161
Db		328	CACCTTACAGGAGGTCATTCGGGCACTAACCCGGGGTCTCTTTCAGGACCAAGCAGAGCAG	269
OY		1162	TGGGCGCGCTCTTGTGTGAGGGGAGCCCGGCTTCACCAACACACATTCGCGCCCTTAGA	1221
Db		268	TGGGCGCGCTCTTGTGTGAGGGGAGCCCGGCTTCACCAAMACACATTCGCGCCCTTAGA	209
OY		1222	GAGCGCAGCCATCTGAGCAAAAGAGAAGATTAACAAGAAAGACACCTCTTATAGGTC	1281
Db		208	GAGCGCAGCCATCTGAGCAAAAGAGAAGATTAACAAGAAAGACACCTCTTATAGGTC	149
OY		1282	CCAAGGGGGCGGGGCTGGGGCTGCGCTAAGTGAAGAAAGCAG	1321
Db		148	CCAAGGGGGCGGGGCTGGGGCTGCGCTAAGTGAAGAAAGCAG	109

RESULT 10
AL558882
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AL558882 Homo sapiens 897 bp mRNA linear EST 02-APR-2004
AL558882 Homo sapiens T CELLS (TOKUAT CELL LINE) COT 10-NORMALIZED
Homo sapiens cDNA clone CSDD015F12.5-PRIME, mRNA sequence.
AL558882
AL558882.3 GI:46184269
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 897)
Li, W.B., Gruber, C., Jesssee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31283015.
Contact: Genoscope

Genoscope - Centre National de Séquençage
2 rue Gaston Cremieux. CP 5706 - 91057 Evry cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalised. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
9945.r
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?b=CS0DJ015DC06Q1&c=9945.r>.
Location/Qualifiers
1. .897
/coordinates="Homo sapiens"

ORIGIN

Query Match	54.1%	Score 714.6;	DB 1;	Length 897;
Best Local Similarity	99.3%	Pred. No. 7.8e-123;		
Matches 736;	Conservative 2;	Mismatches 1;	Indels 2;	Gaps 2;

OY	581	GTGATATCAGTCCCTGCTGAGAGCCACTTACAAAGTGTCTGACAGTCTCTTATATAGTCCGAC	84
Db	1	GTGATATCAGTCCCTGCTGAGAGCCACTTACAAAGTGTCTCTACAGTCTCTTATATAGCCGAC	60
OY	641	AGCCAGGGGCGSAGAGAGAGATAGCCCTGTGCTCAGAAAGATAGCTGTGGCCCTCGSAG	700
Db	61	AGCCAGGGGCGSAGAGAGAGATAGCCCTGTGCTCAGAAAGATAGCTGTGGCCCTCGSAG	120
OY	701	AGCAGATGTTCAGGCAACGGATCCCAAGGCCGAGGTCTACGCCGCCGCTCGGCCAC	760
Db	121	AGCAGATGTTCAGGCAACGGATCCCAAGGCCGAG-GTCTAGCCGCCGCTCGGCCAC	179
OY	761	GACCGCCCTGGGCGCTGTGCGCCCTTTGGGCCAGGGGGAGGGCTTCCACCGCTTCCAGCCAC	820
Db	180	GACCGCCCTGGGCGCTGTGCGCCCTTTGGGCCAGGGGGAGGGCTTCCACCGCTTCCAGCCAC	239
OY	821	TATCCGTATCTGACAGACGAGATGACCTGTGCCACCCACATCTGCTGTCAAGCGGGAG	880
Db	240	TATCCGTATCTGACAGACGAGATGACCTGTGCCACCCACATCTGCTGTCAAGCGGGAG	299
OY	881	GAGCCCCCACCCTTACAGGGGCCCTTGACCTCTCAAGCTTGGGGACCCCGAGACACAGCTG	940
Db	300	GAGCCCCCACCCTTACAGGGGCCCTTGACCTCTCAAGCTTGGGGACCCCGAGACACAGCTG	359
OY	941	GAACTGAACCGGGAGTGCGTGCTGCGGCACCCGCCAACAAGAACATCTTTCAGACGTGACTG	1000
Db	360	GAACTGAACCGGGAGTGCGTGCTGCGGCACCCGCCAACAAGAACATCTTTCAGACGTGACTG	419
OY	1001	ATGATATAGTCCAGAGCTGGGCGGCGCCCTGTGCCCCCAGACAGTAACTGGGGCATACAGGCC	1066
Db	420	ATGATATAGTCCAGAGCTGGGCGGCGCCCTGTGCCCCCAGACAGTAACTGGGGCATACAGGCC	479
OY	1061	ACGTGCTACCGCAGCGGCGGGCGCATGAGAGGGGCGCGGCCACTTACAGGAGGTATCT	1120
Db	480	ACGTGCTACCGCAGCGGCGGGCGCATGAGAGGGGCGCGGCCACTTACAGGAGGTATCT	539
OY	1121	GAGCAGTACCCGGGGTCTCTCTTCAGACCCAGACAGACAGTGGGGCGGCTCTTGTG	1180
Db	540	GAGCAGTACCCGGGGTCTCTCTTCAGACCCAGACAGACAGTGGGGCGGCTCTTGTG	599
OY	1181	GAGGAGACCCGGGCTTCAACACACATTCGCGCCCTTAGAGACCGACCATCTGAGG	1240

QY 762 ACCGCTGGCCGTGCGCCCTTCCAGCGGAGGCGCTTCCAGCCGCTTCCAGCCCACT 821
 Db 266 NNN 325
 QY 822 ATCCGTAAGTGCAGCAGATGAGTGCATCCCACTTCTGCTGTGAGAGGGAGG 881
 Db 326 NNN 385
 QY 882 AGCCCCCACTTACAGAGGCGCCCTGCACTCTCCAGCTTCCGAGCCCGAGCAGAGCTG 941
 Db 386 AGCCCCCACTTACAGAGGCGCCCTGCACTCTCCAGCTTCCGAGCCCGAGCAGAGCTG 445
 QY 942 AACTGAACCGGAGTGTGCGCGCACCCCAACAGAACCATCTTGTGACAGTACTGA 1001
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 QY 1002 TGGATAGTGCAGAGCTGAGGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 1061
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 QY 1062 CGTGTACAGGCGAGGCGGCGGCGATGAGAGGCGCGCCCACTTACAGAGGCTCATG 1121
 Db 566 CGTGTACAGGCGAGGCGGCGGCGATGAGAGGCGCGCCCACTTACAGAGGCTCATG 625
 QY 1122 GCCACTACCGCGGCTCTCTTCCAGCAGCAGAGAGTGGCGCGCTCTTCTGCTG 1181
 Db 626 GCCACTACCGCGGCTCTCTTCCAGCAGCAGAGAGTGGCGCGCTCTTCTGCTG 685
 QY 1182 AGGAGACCGGCTCTTCCAGCAGCAGATGCGCGCTTGAAGAGGCGAGCCATCTGAGCA 1241
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 Db 746 AAGAGAGATTAACAGAAAGACACCTCTCTAG 780

RESULT 14
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 LOCUS 647 bp mRNA linear EST 17-MAY-2005
 DEFINITION TC124411 Human adult whole brain, large insert, PCMV expression
 library Homo sapiens cDNA clone TC124411 5' similar to Homo sapiens
 transmembrane, prostate androgen induced RNA (TMPSAI), transcript
 variant 4, mRNA sequence.
 DN992322
 ACCESSION DN992322.1 GI:66252153
 VERSION EST.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;
 Eukaryota; Metazoa; Eumetazoa; Eumetazoa; Eumetazoa; Eumetazoa;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo
 1 (bases 1 to 647)
 Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L.,
 Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M.,
 Zhang,X., Jay,G. and He,W.
 High-throughput cloning of full-length human cDNAs directly from
 cDNA libraries optimized for large and rare transcripts
 Unpublished (2005)
 Contact: Kovacs, KF
 High Throughput cDNA Cloning
 Origene Technologies, Inc. (www.origene.com)
 6 Taft Court, Suite 100, Rockville, MD 20850, USA
 Tel: 301 340 3188
 Fax: 301 340 8606
 Email: cdna@origene.com
 This EST submission is part of an on-going human full-length
 cloning project at Origene Technologies, Inc.
 Please contact Origene for access.
 Origene Technologies, Inc.
 6 Taft Ct, Suite 100
 Rockville, MD 20850

Tel: (301) 340-3188
 http://www.origene.com
 Seq primer: PCMV6 5prime forward vector primer, Origene
 Technologies Inc.
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="TC124411"
 /issue_type="Whole brain"
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 expression library"
 /note="Organ: Brain; Vector: pCMV6-XL5; Site 1: EcoRI;
 Site 2: XhoI/SalI compatible end ligato; Oligo-dT primed
 reverse transcription optimized for large and GC rich mRNA
 transcripts, cDNA size selection, optimized ligation for
 large inserts into mammalian expression vector, random
 clones selected for end sequence verification of
 full-length genes"

ORIGIN
 Query Match 48.3%; Score 637.4; DB 8; Length 647;
 Best Local Similarity 99.8%; Pred. No. 1.8e-108;
 Matches 638; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 420 GCTTGTAGGAGGCTCAACAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 479
 Db 9 GCTTGTAGGAGGCTCAACAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 68
 QY 480 CGTGCAATGCAAAAGCTCTTGTTCAGAGCATGAGATCAAGAGTGAAGTGAAGTGAAG 539
 Db 69 CGTGCAATGCAAAAGCTCTTGTTCAGAGCATGAGATCAAGAGTGAAGTGAAGTGAAG 128
 QY 540 AGATCATCATCATCGT 599
 Db 129 AGATCATCATCATCGT 188
 QY 600 GCCACTAACAGCTGT 659
 Db 189 GCCACTAACAGCTGT 248
 QY 660 AAGATGCCCTGTCTTCAAGAGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 719
 Db 249 AAGATGCCCTGTCTTCAAGAGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 308
 QY 720 GAATCCAGAGCGCAGGTCTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 779
 Db 309 GAATCCAGAGCGCAGGTCTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 368
 QY 780 CTTTGGCCAGCGGAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTT 839
 Db 369 CTTTGGCCAGCGGAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGCTT 428
 QY 840 AGATCCAGCTTCCAGCG 899
 Db 429 AGATCCAGCTTCCAGCG 488
 QY 900 GCCCTGCACTTCCAGCG 959
 Db 489 GCCCTGCACTTCCAGCG 548
 QY 960 TGGCGGACCGCCCAACAGAACCATCTTGTGACAGTGAAGTGAAGTGAAGTGAAGTGA 1019
 Db 549 TGGCGGACCGCCCAACAGAACCATCTTGTGACAGTGAAGTGAAGTGAAGTGAAGTGA 608
 QY 1020 GCGGCG 1058
 Db 609 GCGGCG 647

RESULT 15
 CU028468

Db	271	CTCGAAGAGCACAAGTGTCAAGGCAACGGAATCCAGAGCCGACAGTCTACGCCCCCTTCG	330
QY	754	GCCCAACCGACCGCTCGTGGCCGTGCGCCCTTTGGCCCAAGTGGAGCGCTTCAACCGCTTCA	813
Db	331	GCCCAACCGACCGCTCGTGGCCGTGCGCCCTTTGGCCCAAGTGGAGCGCTTCAACCGCTTCA	390
QY	814	GCCCAACCTATCCGTACTGACAGCAGAGATGCACTGCAACCAACATCTCGTGTGAGA	873
Db	391	GCCCAACCTATCCGTACTGACAGCAGAGATGCACTGCAACCAACATCTCGTGTGAGA	450
QY	874	CGGGAGGAGGCCCCCAACCTTACAGAGGCCCTTGACCTTCCAGCTTGGGAACTCCGAGCA	933
Db	451	CGGGAGGAGGCCCCCAACCTTACAGAGGCCCTTGACCTTCCAGCTTGGGAACTCCGAGCA	510
QY	934	GCAGCTGGAATGAAACCGGAGAGTGCGTGGCGGCAACCCCAACAGAACATCTTGCAGAG	993
Db	511	GCAGCTGGAATGAAACCGGAGAGTGCGTGGCGGCAACCCCAACAGAACATCTTGCAGAG	570
QY	994	TGACCTGATGATAGTATGTCACAGGCTGGGCGGCCCTTCCAGACCAAGTAACTCGGAGCAT	1057
Db	571	TGACCTGATGATAGTATGTCACAGGCTGGGCGGCCCTTCCAGACCAAGTAACTCGGAGCAT	630
QY	1054	CAGGCGCAACGTGCTAAGCGGCAAGCGGGGGCGATGGAAGGGGGCGCGGCCCACTTACAGGGA	1111
Db	631	CAGGCGCAACGTGCTAAGCGGCAAGCGGGGGCGATGGAAGGGGGCGCGGCCCACTTACAGGGA	690
QY	1114	GGTATCTGGGCACTACACCGCGGGTCTCTCTTCCAGACCAAGCAGAGCAATGGGCGGCTCTC	1177
Db	691	GGTATCTGGGCACTACACCGCGGGTCTCTCTTCCAGACCAAGCAGAGCAATGGGCGGCTCTC	750
QY	1174	CTTGTGTGAGGGAGGACCGCGCTCCACACACACACACACATCGCGGCCCTTAAAGAGGGCAGCCAT	1237
Db	751	CTTGTGTGAGGGAGGACCGCGCTCCACACACACACACACATCGCGGCCCTTAAAGAGGGCAGCCAT	810
QY	1234	CTGGAGCAAAAGAGAGATTAACAGAAAGGACACCTCTCTTAAGGGTCCCAAGGGGGCCG	1297
Db	811	CTGGAGCAAAAGAGAGATTAACAGAAAGGACACCTCTCTTAAGGGTCCCAAGGGGGCCG	870
QY	1294	GGCTGGGGCTGCTGTGCTGTAAGGACAG	1321
Db	871	GGCTGGGGCTGCTGTGCTGTAAGGACAG	898
RESULT 2			
US-09-769-482-2			
Sequence 2, Application US/09769482			
Patent No. 6566130			
GENERAL INFORMATION:			
APPLICANT: SRIVASTAVA, SHIV			
APPLICANT: MOUL, JUDD W.			
APPLICANT: XU, LINDA L.			
APPLICANT: SEGAWA, TAKEHIKO			
TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED			
FILE REFERENCE: 04995, 0057-0000			
CURRENT FILING DATE: 2001-01-26			
PRIOR FILING DATE: 2000-01-28			
PRIOR APPLICATION NUMBER: 60/179, 772			
PRIOR FILING DATE: 2000-01-28			
PRIOR APPLICATION NUMBER: 60/179, 045			
NUMBER OF SEQ ID NOS: 67			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO 2			
LENGTH: 759			
TYPE: DNA			
ORGANISM: Homo sapiens			
US-09-769-482-2			

OY		518	ATCACGAGCTGGAGGTGTTTCATCATCATCATCCTGTGTGGTGAATGATGATGGTG	577
Dd		1	ATGCCGAGCTGGAGTGTGTTCAAGTATCATCATCGTGTGGTGAATGATGATGGTG	60
OY		578	GTCGTGATCACTGTCCTGTGAGCCACTACAGCTGTCTGCACGGTCTTTCATCAGCCGG	637
Dd		61	GTGGTGTATCACTGTGCTGTGAGCCACTACAGCTGTCTGCACGGTCTTTCATCAGCCGG	120
OY		638	CACAGCCAGGGGCGGAGAGAGAAGATGCCCTGTGCTCACAAGGATGCTGTGGCCCTCG	697
Dd		121	CACAGCCAGGGGCGGAGAGAGAAGATGCCCTGTGCTCACAAGGATGCTGTGGCCCTCG	180
OY		698	GAGAGCACAAGTGTGAGGCAAAGAAATCCCAAGGCGGAGGTCTTAAGCCCCGCTCGACC	757
Dd		181	GAGAGCACAAGTGTGAGGCAAAGAAATCCCAAGGCGGAGGTCTTAAGCCCCGCTCGACC	240
OY		758	ACCGAGCCGCTGAGCCGTGTCGCCCTTTCGCCACGAGGAGCGCTTTCACCCGCTTCAAGCCC	817
Dd		241	ACCGAGCCGCTGAGCCGTGTCGCCCTTTCGCCACGAGGAGCGCTTTCACCCGCTTCAAGCCC	300
OY		818	ACCTATCCGTAACCTGACAGCACAGATATGACTGTGCACCCACATCTGTGCTGAGAGGG	877
Dd		301	ACCTATCCGTAACCTGACAGCACAGATATGACTGTGCACCCACATCTGTGCTGAGAGGG	360
OY		878	GAGAGGCCCCCACCCTACAGAGGGGCCCTTGACCTTCAGATTGCGGAGACCCGAGACAG	937
Dd		361	GAGAGGCCCCCACCCTACAGAGGGGCCCTTGACCTTCAGATTGCGGAGACCCGAGACAG	420
OY		938	CTGGAACCTGAACCGGAGATCGGTGCGCGCACCCGCCAACAAGAACCTATCTTGACAGTGAC	997
Dd		421	CTGGAACCTGAACCGGAGATCGGTGCGCGCACCCGCCAACAAGAACCTATCTTGACAGTGAC	480
OY		998	CTGATGTGATATGTGCCAAGCTGTGGGGGGCCCTTGCCCCCAGCAGATACTGGGGGATAGC	1057
Dd		481	CTGATGTGATATGTGCCAAGCTGTGGGGGGCCCTTGCCCCCAGCAGATACTGGGGGATAGC	540
OY		1058	GCCAGTGTCTACGGCAGCGGCGGCGCATGTGAGGGGCGCGCCACCTACAGAGGAGTC	1117
Dd		541	GCCAGTGTCTACGGCAGCGGCGGCGCATGTGAGGGGCGCGCCACCTACAGAGGAGTC	600
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Dd		601	ATCGGCACTACCCCGGGGTCTCTCTTCACAGCACAGCAGCAGTAGTGGAGCGGCTCTTGG	660
OY		1178	CTGAGAGGGGACCCGGCTTCACACACACACATGCGGCCCTTAGAGAGCGCAGCATCTGG	1237
Dd		661	CTGAGAGGGGACCCGGCTTCACACACACACATGCGGCCCTTAGAGAGCGCAGCATCTGG	720
OY		1238	AGCAAAAGAGATTAACAGAAAAGACACCCTCTTAG	1276
Dd		721	AGCAAAAGAGATTAACAGAAAAGACACCCTCTTAG	759
RESULT 3				
US-09-091-952A-7				
Sequence 7, Application US/09091952A				
Patent No. 6458532				
GENERAL INFORMATION:				
APPLICANT: Deterra-Wadleigh, Sevilla D.				
Gershon, Elliot S.				
Badner, Judith A.				
Goldin, Lynn R.				
Berretini, Wade H.				
Yoshikawa, Takeo				
Sanders, Alan R.				
Esterling, Lisa B.				
TITLE OF INVENTION: Chromosomal Markers and Diagnostic Tests for Manic-Depressive Illness				
NUMBER OF SEQUENCES: 197				
CORRESPONDENCE ADDRESS:				
ADDRESS: Townsend and Townsend and Crew LLP				
STREET: Two Embarcadero Center, Eighth Floor				
CITY: San Francisco				


```

STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,952A
FILING DATE: 19-Apr-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,278
FILING DATE: 28-OCT-1996
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 015280-297100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 921 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1...921
OTHER INFORMATION: Clone 22 coding region
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-091-952A-7

Query Match      26.7%; Score 352.2; DB 3; Length 921;
Best Local Similarity 73.1%; Pred. No. 1.9e-57;
Matches 482; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

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QY      986 TTGCACATGACCTGATGATAGTGCAGG---CTGGCGGCGCCCTGCGCCCGCAGCAGT 1042
DB      640 TTTCACATGATTTAATAGCATTTGCTATGATAGCGGGGGTTCATGCCCCACCGAC 699
QY      1043 AACTGGGCGATCAGGCGCCACGCTACGAGCGCGCGGCAGATGAGAGGGCGCGCGCC 1102
DB      700 AACTGGGCGATCAGTGCAGACCGCTGACAGCAGTAAAGGAGATGAGAGGGCGCACCC 759
QY      1103 AACTACAGCAGAGTATCGGCGCATACCGGGGCTCTCTTCAGACACCGACGACGAG 1161
DB      760 ACATACAGGAGGTATGAGGCGCACCAACGAGCGCTCTTCTCCTCATCAGCGGCGAG 818

RESULT 4
US-09-091-952A-6
Sequence 6, Application US/09091952A
Patent No. 6458532
GENERAL INFORMATION:
APPLICANT: DeCera-Wadleigh, Sevilla D.
Gershon, Elliot S.
Badner, Judith A.
Goldin, Lynn R.
Berretini, Wade H.
Yoshikawa, Takeo
Sanders, Alan R.
Besterling, Lisa E.
TITLE OF INVENTION: Chromosomal Markers and Diagnostic
Tests for Manic-Depressive Illness
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,952A
FILING DATE: 19-Apr-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,278
FILING DATE: 28-OCT-1996
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 015280-297100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8065 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY:
LOCATION: 1...8065
OTHER INFORMATION: Clone 22
NAME/KEY: CDS

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LOCATION: 116..1036
OTHER INFORMATION: Clone 22 coding region
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  LOCATION: 452...505
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  LOCATION: 5595...5685
OTHER INFORMATION: amplified region for genotyping
SEQUENCE DESCRIPTION: SEQ ID NO: 6
US-09-091-952A-6

Query Match      26.7%; Score 352.2; DB 3; Length 8065;
Best Local Similarity 73.1%; Pred. No. 2,4e-57;
Matches 482; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

QY 506 CAGACGATGAGATCAGCGAGCTGGAGTTTGTTCAGATCATCATCATGCTGCTGATG 565
DB 281 CCGGCACTTCTAATCTCGAGCTGGAGTTTCGCCCAATCATCATCATGCTGCTGATG 340
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QY 626 TTTCATCAGCCGACACGAGGCGGAGAGAGAGAGATGCTCTGCTCAGAGAGATG 685
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QY 686 CTGTGAGCCCTGGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATG 745
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RESULT 5
US-09-311-021-65
; Sequence 65, Application US/09111021
; Patent No. 6706869
GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Recheil, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
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FILE REFERENCE: GI 6300-11A
CURRENT APPLICATION NUMBER: US/09/311,021
CURRENT FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 268
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 65
LENGTH: 937
TYPE: DNA
ORGANISM: Homo sapiens
US-09-311-021-65

Query Match      26.6%; Score 351.6; DB 3; Length 937;
Best Local Similarity 73.0%; Pred. No. 2,4e-57;
Matches 482; Conservative 0; Mismatches 169; Indels 9; Gaps 2;

QY 505 CCAGAGATGAGATCAGCGAGCTGGAGTTTGTTCAGATCATCATCATGCTGCTGATG 564
DB 134 CTTGTTCTTAAAAAAGCGAGGCTGGAGTTTCGCCCAATCATCATCATGCTGCTGATG 193
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DB 254 CTTTCATCAGCCGACACGAGGCGGAGAGAGAGATGCTCTGCTCAGAGAGATG 313
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DB 368 TCGCGCGGCTTCAGAGGACAGGTTTCAAGGCGGCTTTCATCAGAGGAGATGCTTTCAG 427
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DB 428 CCGCTTCAGAGCCCACTTATCTGATGATGATGATGATGATGATGATGATGATG 487
QY 865 CCGTTCAGAGCCCACTTATCTGATGATGATGATGATGATGATGATGATGATG 924
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DB 985 CCGGAGAGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 607
QY 548 CCGTTCAGAGCCCACTTATCTGATGATGATGATGATGATGATGATGATGATG 607
DB 607 CCGTTCAGAGCCCACTTATCTGATGATGATGATGATGATGATGATGATGATG 667
QY 985 CTTTCAGAGCCGACACGAGGCGGAGAGAGATGCTCTGCTCAGAGAGATG 1041
DB 608 ATTTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 667
QY 1042 TTAATCGGAGATCAGCGGCGCCGCTGCTAAGGAGCGGCGGCGGCGGCGGCGGCGG 1101
DB 668 CAATCGGAGATCAGCGGCGCCGCTGCTAAGGAGCGGCGGCGGCGGCGGCGGCGG 727
QY 1102 CAATCGGAGATCAGCGGCGCCGCTGCTAAGGAGCGGCGGCGGCGGCGGCGGCGG 1161
DB 728 CAATCGGAGATCAGCGGCGCCGCTGCTAAGGAGCGGCGGCGGCGGCGGCGGCGG 787

RESULT 6
US-09-091-952A-8
; Sequence 8, Application US/09091952A
; Patent No. 6458532
GENERAL INFORMATION:
; APPLICANT: Deterra-Wadleigh, Sevilla D.
; APPLICANT: Gershon, Elliot S.
; APPLICANT: Badner, Judith A.
; APPLICANT: Goldin, Lynn R.
; APPLICANT: Berreilini, Wade H.
; APPLICANT: Yoshikawa, Takeo
; APPLICANT: Sanders, Alan R.
; APPLICANT: Beterling, Lisa E.
```


Query Match	5.7%	Score 75.4	DB 3	Length 2561
Best Local Similarity	53.0%	Pred. No. 2.7e-05		
Matches 206; Conservative		0; Mismatches 181	Indels 2	Gaps 2

RESULT 9
US-09-976-740-48/c
; Sequence 48, Application US/09976740

PRIOR APPLICATION NUMBER: 09/616,289

Query Match	5.7%	Score 75.4	DB 3	Length 2561
Best Local Similarity	53.0%	Pred. No. 2.7e-05		
Matches 206; Conservative	0	Mismatches 181	Indels 2	Gaps 2

RESULT 10
US-09-616-289-48
; Sequence 48, Application US/09616289
; Patent No. 6632923

PRIOR APPLICATION NUMBER: US 60/048,547

LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 5.2%; Score 68.8; DB 3; Length 4411529;
Best Local Similarity 49.8%; Pred. No. 0.0014;
Matches 229; Conservative 0; Mismatches 227; Indels 4; Gaps 2;

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QY      2  GACCGGCTCTCGAGAGCAACCCGATCTCTTGACTTGAATGAGAGAGAGGCGGC 61
Db      3942788  GCCGGGCGCAACGCGCGCACCGCGCAAGAGCGGCACTGTGGCGCCCGCGGCAAGGT 3942847
QY      62  GCGCGCGCGCGCGCGCGAGGCGCTCGGAGAAAGCTAGCGGCAAGGCTCAGCCCG 121
Db      3942848  ATCGGTGGGTGGCGCGCGCGCAAGCGGCAACGCGCGGCAACGCGCGGAGTCCGCGGTGCG 3942907
QY      122  GCGGCAAGCGCGCGCGCGCTGCTCAGCCATTTCGGAAGCCACCCCGCGGCACTGCCG 180
Db      3942908  GCGGCGCGCGCGCGCGCGCAACACAGTCCGCGCGCAACGCGCGGCAAGAGGT 3942967
QY      181  -ACGCGCGCGCGCGCTGCGAGAGGAGCGGCGCGCGCGCGAGCGGCGGCTCCCGCA 239
Db      3942968  CAAAGCGGCAACGCTGTGTGCGGTGGGCGCGCGCGCTGCGCGCGCGCGCT 3943027
QY      240  CTGAGCGCGCGCGCGCGCGGAACTTGGCGCGGACCCGAGCCCGGCAAGCGCGCGCG 299
Db      3943028  AACGGCAACGCTGGCAACGCGCGCGCAAGGCGGTGCGCGCGCAACGCGCGCGCGCA 3943087
QY      300  CTTCCCGCGCGCGCGCTCTCTGCAATGCGGAGCCCACTCCGCGCGCGCGCGAGCC 359
Db      3943088  GCCTCTCAGCTACCAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3943145
QY      360  CCGCGCGCGCGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 419
Db      3943146  GCAAGCGCGCGCGCGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3943205
QY      420  GCTTGATGGGAGTCAACAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 459
Db      3943206  GCGGACAGGTGCGCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3943245
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Search completed: February 28, 2006, 12:29:25
Job time : 273.59 secs

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Db 181 AGCCCCCGGGGCTGCCAGAGGGAGCCGGGGGGCGCAGCGGAGCGCGTCCCGGCAC 240
Qy 241 TGAGCCCCCGGGGCTGCCAGAGGGAGCTTTGCGCGCAGCCCGAGCCCGGGGCGCGC 300
Db 241 TGAGCCCCCGGGGCTGCCAGAGGGAGCTTTGCGCGCAGCCCGAGCCCGGGGCGCGC 300
Qy 301 CTTCCCCCGGGGCTGCCAGAGGGAGCCCGAGCGTCCGGGGGGCGGGAGCCCC 360
Db 301 CTTCCCCCGGGGCTGCCAGAGGGAGCCCGAGCGTCCGGGGGGCGGGAGCCCC 360
Qy 361 CCCCCGGGCGCCCCGAGCCCCCGGGCGCGCGCGCGCGCGCGCTGCATGACCG 420
Db 361 CCCCCGGGCGCCCCGAGCCCCCGGGCGCGCGCGCGCGCGCGCTGCATGACCG 420
Qy 421 CTTGATGGGGGTCAACAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 480
Db 421 CTTGATGGGGGTCAACAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 480
Qy 481 GTGCACTGCAAAAGCTTTTGTTCAGAGCAATGAGATCAGGAGCTGGAATTTGTTCA 540
Db 481 GTGCACTGCAAAAGCTTTTGTTCAGAGCAATGAGATCAGGAGCTGGAATTTGTTCA 540
Qy 541 GATCATCATCATCGT 600
Db 541 GATCATCATCATCGT 600
Qy 601 CCACTAACAAGCTGT 660
Db 601 CCACTAACAAGCTGT 660
Qy 661 AGATGCGCTGTCTCTCAAGAGAGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Db 661 AGATGCGCTGTCTCTCAAGAGAGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Qy 721 AATCCAGAGCGCAGGTCTAGCGCCCGGCTCGGCCCAACCGCGCTGCGCGCGC 780
Db 721 AATCCAGAGCGCAGGTCTAGCGCCCGGCTCGGCCCAACCGCGCTGCGCGCGC 780
Qy 781 CTTTGGCCAGCGGAGCGCTTCCAGCGCTTCCAGCCCTATCCGTACCTGACAGCA 840
Db 781 CTTTGGCCAGCGGAGCGCTTCCAGCGCTTCCAGCCCTATCCGTACCTGACAGCA 840
Qy 841 GATCGACTGCGCCACCACTTCGCTGTCAAGCGGGAGAGAGCCCGCCCTACCAAGG 900
Db 841 GATCGACTGCGCCACCACTTCGCTGTCAAGCGGGAGAGAGCCCGCCCTACCAAGG 900
Qy 901 CCCCTCACTCTCACTTCGAGCCCGAGCAGAGCTGGAAGTGAACCGGGAGTCCGT 960
Db 901 CCCCTCACTCTCACTTCGAGCCCGAGCAGAGCTGGAAGTGAACCGGGAGTCCGT 960
Qy 961 GCGGCGACCCCAAGAACATCTTTCAGACTGACCTGTATGATGTCAGGCTGGG 1020
Db 961 GCGGCGACCCCAAGAACATCTTTCAGACTGACCTGTATGATGTCAGGCTGGG 1020
Qy 1021 CCGGCCCCCTGCCCCAGAGTAACTCGGGCATCAAGCGCTGTACGCGCGCGG 1080
Db 1021 CCGGCCCCCTGCCCCAGAGTAACTCGGGCATCAAGCGCTGTACGCGCGCGG 1080
Qy 1081 GCGCATGAGAGGGCGCGCGCCACCTACAGCGAGTCACTGCGGCTGCTC 1140
Db 1081 GCGCATGAGAGGGCGCGCGCCACCTACAGCGAGTCACTGCGGCTGCTC 1140
Qy 1141 CTTTCAAGCAGCAGAGAGAGTGGCGCGCTTCTTGTGAGAGGGAGCCCGGCTCCACA 1200
Db 1141 CTTTCAAGCAGCAGAGAGAGTGGCGCGCTTCTTGTGAGAGGGAGCCCGGCTCCACA 1200
Qy 1201 CACACACATGCGCCCTTAAAGAGCGAGCATCTGAGCAAGAAAGAAAGTAAACAGAA 1260
Db 1201 CACACACATGCGCCCTTAAAGAGCGAGCATCTGAGCAAGAAAGAAAGTAAACAGAA 1260
Qy 1261 AGGACACCTCTCTAAGGGTCCCGAGGGGGGCGGGGCTGCGTAAAGAGCA 1320
Db 1261 AGGACACCTCTCTAAGGGTCCCGAGGGGGGCGGGGCTGCGTAAAGAGCA 1320

Qy 1321 G 1321
Db 1321 G 1321

RESULT 2
US-10-241-220-119
; Sequence 119, Application US/10241220
; Publication No. US20030148408A1
; GENERAL INFORMATION:
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5010R1-US
; CURRENT APPLICATION NUMBER: US/10/241, 220
; CURRENT FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 119
; LENGTH: 4839
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-241-220-119

Query Match 93.0%; Score 1229; DB 6; Length 4839;
Best Local Similarity 100.0%; Pred. No. 8,9e-288; Mismatches 0; Indels 0; Gaps 0;
Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 GGAAGCTAGCGGAGAGGCTCAAGCCCGGCGGAGCGCGCCCGCTGCAAGCCATT 152
Db 1 GGAAGCTAGCGGAGAGGCTCAAGCCCGGCGGAGCGCGCCCGCTGCAAGCCATT 60
Qy 153 TTCCGAGCGCACCCCGCGGCACTGCGCAGCGCCCGGGGCTGCGAGAGGCGCGGG 212
Db 61 TTCCGAGCGCACCCCGCGGCACTGCGCAGCGCCCGGGGCTGCGAGAGGCGCGGG 120
Qy 213 GGGCGCAGCGAGCGCGGCTCCCGGCACTGAGCCCGCGGCGCGCCCGGAACTTGGCGGC 272
Db 121 GGGCGCAGCGAGCGCGGCTCCCGGCACTGAGCCCGCGGCGCGCCCGGAACTTGGCGGC 180
Qy 273 GACCCGAGCCCGGCGAGCGGGGCGCGCTCCCGCGCGCGCGCTCTGATGCGGGG 332
Db 181 GACCCGAGCCCGGCGAGCGGGGCGCGCTCCCGCGCGCGCGCTCTGATGCGGGG 240
Qy 333 CCGAGCTCGGGCGCGCGCGCGAGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCG 392
Db 241 CCGAGCTCGGGCGCGCGCGCGAGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCG 300
Qy 393 GCGGCG 452
Db 301 GCGGCG 360
Qy 453 CCGCGGCGAGCCCAATGCTCTGCGAGCTGCAAGTGAACGCTTTGTTTCCAGAGCA 512
Db 361 CCGCGGCGAGCCCAATGCTCTGCGAGCTGCAAGTGAACGCTTTGTTTCCAGAGCA 420
Qy 513 TGAAGATCAAGAGCTGAGATTGTTTCAAGTATCATATGTTGTTGATGATGATGATG 572
Db 421 TGAAGATCAAGAGCTGAGATTGTTTCAAGTATCATATGTTGTTGATGATGATGATG 480
Qy 573 TGTGTGTGTATCAAGTGTGCGCGCGAGCGCACTAAGAGTGTCTGACAGGTCCTCATCA 632
Db 481 TGTGTGTGTATCAAGTGTGCGCGCGAGCGCACTAAGAGTGTCTGACAGGTCCTCATCA 540
Qy 633 GCCGCAAGCGAGGGGCGAGAGAGAGTATGCTGTCTCTCAAGAGATGCTGTGGC 692

Db 1021 AGGTATGAGCCACTACCCGGGGTCTCTTCCAGACCAAGAGAGAGTGGCCCT 1080
Qy 1173 CCTTCTGGAGGAGGAGCCCGGCTCCACACACACATGCGCCCTTAGAGAGGAGCCA 1232
Db 1081 CCTTCTGGAGGAGGAGCCCGGCTCCACACACACATGCGCCCTTAGAGAGGAGCCA 1140
Qy 1233 TCTGAGCAAGAGAGATTAACAGAAAGAGACCTCTCTAGAGTCCCGGAGGGGCC 1292
Db 1141 TCTGAGCAAGAGAGATTAACAGAAAGAGACCTCTCTAGAGTCCCGGAGGGGCC 1200
Qy 1293 GGGCTGGGGCTGCTAGTGAAGAGAGAG 1321
Db 1201 GGGCTGGGGCTGCTAGTGAAGAGAGAG 1229

RESULT 4
US-10-269-909-85
Sequence 85, Application US/10269909
Publication No. US20030180747A1
GENERAL INFORMATION:
APPLICANT: HRUBAN, RALPH H.
APPLICANT: ARGANI, PEDRAM
APPLICANT: IACOBUIZIO-DONAHUE, CHRISTINE
APPLICANT: MAITRA, ANIRBAN
TITLE OF INVENTION: PANCREATIC CANCER DIAGNOSIS AND THERAPIES
FILE REFERENCE: 58303(71699)
CURRENT APPLICATION NUMBER: US/10/269,909
PRIOR FILING DATE: 2003-10-11
PRIOR APPLICATION NUMBER: 60/328,609
PRIOR FILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: 60/332,754
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 85
LENGTH: 4839
TYPE: DNA
ORGANISM: Homo sapiens
US-10-269-909-85

Query Match 93.0%; Score 1229; DB 6; Length 4839;
Best Local Similarity 100.0%; Pred. No. 8,9e-288;
Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 GGAAGCTAGCGGACAGAGGCTCAGCCCGCGGACAGCGCGCCCGCTGACAGCCACT 152
Db 1 GGAAGCTAGCGGACAGAGGCTCAGCCCGCGGACAGCGCGCCCGCTGACAGCCACT 60
Qy 153 TTCGGACGCGACCCCGGGGCACTGCCAGCGCCCGGGGCTTCCGAGGGAGAGCCGGG 212
Db 61 TTCGGACGCGACCCCGGGGCACTGCCAGCGCCCGGGGCTTCCGAGGGAGAGCCGGG 120
Qy 213 GGGCGAGGAGGAGCGGGGTCGGCGGCACTGAGGCCCGCGGCGCCCGGGAACTTGGCGG 272
Db 121 GGGCGAGGAGGAGCGGGGTCGGCGGCACTGAGGCCCGCGGCGCCCGGGAACTTGGCGG 180
Qy 273 GACCCGAGCCCGGAGCCCGGGGCGGCTCCCGCGCGCGCTCTGECATGCGAGGCG 332
Db 181 GACCCGAGCCCGGAGCCCGGGGCGGCTCCCGCGCGCGCTCTGECATGCGAGGCG 240
Qy 333 CCCAGCTCCGGGCGCGGGCGGAGCCCGCGCGCGCCCGCGAGCCCGCGCGCGCG 392
Db 241 CCCAGCTCCGGGCGCGGGCGGAGCCCGCGCGCGCCCGCGAGCCCGCGCGCGCG 300
Qy 393 GCGCGCGCGCGCGCGGCTCATGCAACGCTTGAATGGGGGTCACAGACCGCGCGCGG 452
Db 301 GCGCGCGCGCGCGCGGCTCATGCAACGCTTGAATGGGGGTCACAGACCGCGCGCGG 360
Qy 453 CGCGCGGAGAGCCCAATGTCTCTGCACTGCACTGCAACTGCAACGCTCTTTGTTCCAGAGA 512
Db 361 CGCGCGGAGAGCCCAATGTCTCTGCACTGCACTGCAACTGCAACGCTCTTTGTTCCAGAGA 420
Qy 513 TGGAGATCAAGAGAGTGAAGTTTGTTCATGATCATCATCTGTTGGTGGATGATGATGA 572

Db 421 TGGAGATCAAGAGAGTGAAGTTTGTTCATGATCATCATCTGTTGGTGGATGATGATGA 480
Qy 573 TGGTGTGTGTATCATCGTGTCTGTAAGCACTAAGCTGTCTGACAGGCTCTTATCA 632
Db 481 TGGTGTGTGTATCATCGTGTCTGTAAGCACTAAGCTGTCTGACAGGCTCTTATCA 540
Qy 633 GCCGCGACAGCCAGGGCGGAGAGAGATGCTGTCTCTGAAAGATGCTGTGGC 692
Db 541 GCCGCGACAGCCAGGGCGGAGAGAGATGCTGTCTCTGAAAGATGCTGTGGC 600
Qy 693 CCTGAGAGAGACAGTGTCAAGCAAGCAATCCAGAGCCGAGGTCTACGCCGCCCTC 752
Db 601 CCTGAGAGAGACAGTGTCAAGCAAGCAATCCAGAGCCGAGGTCTACGCCGCCCTC 660
Qy 753 GGGCCACGACCGCTGGGCTGTGCGCCCTTCTGCGAGCGGAGAGCTTCCACCGCTTCC 812
Db 661 GGGCCACGACCGCTGGGCTGTGCGCCCTTCTGCGAGCGGAGAGCTTCCACCGCTTCC 720
Qy 813 AGCCCACTATCCGTACCTTGAGAGACAGATGACCTGACCCACCATCTGCGTTCAG 872
Db 721 AGCCCACTATCCGTACCTTGAGAGACAGATGACCTGACCCACCATCTGCGTTCAG 780
Qy 873 AGGGGAGAGAGCCGCCACCTACAGAGGCGCCCTGACCCCTGAGCTTGGAGAGCCGAGC 932
Db 781 AGGGGAGAGAGCCGCCACCTACAGAGGCGCCCTGACCCCTGAGCTTGGAGAGCCGAGC 840
Qy 933 AGCAGCTGAACTGAAACCGGAGTGTGGTGGCGGACCCCGCAAGAACCACTTTTCACA 992
Db 841 AGCAGCTGAACTGAAACCGGAGTGTGGTGGCGGACCCCGCAAGAACCACTTTTCACA 900
Qy 993 GTGACTGATGATAGTGTCCAGGCTGTGGGCGGCGCCCTGCGCCCGCAGAGTAATCTGGGCA 1052
Db 901 GTGACTGATGATAGTGTCCAGGCTGTGGGCGGCGCCCTGCGCCCGCAGAGTAATCTGGGCA 960
Qy 1053 TCAGCGCCACAGTGTCAAGGAGCGGCGGCGCATGAGAGGCGCGCGCCCACTTACAGCG 1112
Db 961 TCAGCGCCACAGTGTCAAGGAGCGGCGGCGCATGAGAGGCGCGCGCCCACTTACAGCG 1020
Qy 1113 AGGTATGAGGCTACCTACCGGGGCTCTCTTTCAGACACAGACAGAGAGTGGGCGCCCT 1172
Db 1021 AGGTATGAGGCTACCTACCGGGGCTCTCTTTCAGACACAGAGAGAGTGGGCGCCCT 1080
Qy 1173 CCTTCTGAGAGGAGACCCGGGCTCCACACACACATGCGCCCTTAGAGAGCGAGCA 1232
Db 1081 CCTTCTGAGAGGAGACCCGGGCTCCACACACACATGCGCCCTTAGAGAGCGAGCA 1140
Qy 1233 TCTGAGCAAGAGAGATTAACAGAAAGAGACCTCTCTAGAGTCCCGGAGGGGCC 1292
Db 1141 TCTGAGCAAGAGAGATTAACAGAAAGAGACCTCTCTAGAGTCCCGGAGGGGCC 1200
Qy 1293 GGGCTGGGGCTGCTAGTGAAGAGAGAG 1321
Db 1201 GGGCTGGGGCTGCTAGTGAAGAGAGAG 1229

RESULT 5
US-10-872-972-119
Sequence 119, Application US/10872972
Publication No. US20040229277A1
GENERAL INFORMATION:
APPLICANT: Franz, Gretchen
APPLICANT: Hillan, Kenneth J.
APPLICANT: Phillips, Heidi
APPLICANT: Polakis, Paul
APPLICANT: Spencer, Susan
APPLICANT: Williams, P. Mickey
APPLICANT: Wu, Thomas
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF TUMOR
FILE REFERENCE: P5010R1-US
CURRENT APPLICATION NUMBER: US/10/872,972

541 GAGTCGGTGGCGCACCCCAACAGAACCATCTTCGACAGTGACCTGATGGATAGTCC 600

PRIOR FILING DATE: 2000-06-22

DB 377 CTTCCACGGCTTCCAGCCCACTTATCCGTAAGTCCAGACGAGATGACCTGACCCAC 436
QY 859 CATCTCGCTGTGACAGCGGGAGAGACCCCACTTACCAAGGCCCCCTGACCTTCAAGT 918
DB 437 CATCTCGCTGTGACAGCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 496
QY 919 TCGGAGACCCCGAGCAGCAGCTGAACTGAACTGAACTGAACTGAACTGAACTGAACTG 978
DB 497 TCGGAGACCCCGAGCAGCAGCTGAACTGAACTGAACTGAACTGAACTGAACTGAACTG 556
QY 979 AACCATCTTCCAGCAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGA 1038
DB 557 AACCATCTTCCAGCAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGA 616
QY 1039 CAGTAATCTGAGGATCAAGGCGCACTGTAAGCGAGCGGCGGCGGCGGCGGCGGCGGCG 1098
DB 617 CAGTAATCTGAGGATCAAGGCGCACTGTAAGCGAGCGGCGGCGGCGGCGGCGGCGGCGG 676
QY 1099 GCGGACCTTCAAGCAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGA 1158
DB 677 GCGGACCTTCAAGCAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGA 736
QY 1159 CAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1218
DB 737 CAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 796
QY 1219 AGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1278
DB 797 AGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 856
QY 1279 TCCCGAGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1321
DB 857 TCCCGAGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 899

RESULT 12

US-10-301-822-208
Sequence 208, Application US/10301822
Publication No. US20030148410A1

GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Bursart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILE REFERENCE: MPM01-029P2RM
CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 208
LENGTH: 1141
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (96)...(854)
US-10-301-822-208

Query Match

60.7%; Score 802.2; DB 6; Length 1141;

Best Local Similarity 98.4%; Pred. No. 1.9e-184;
Matches 810; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 499 TTGTTCAGAGCATGAGATGACGAGCTGAGTTGTGATGATCATCATCATCTGCTGCT 558
DB 77 TGTCTGTGAAACAGAGGAAAGGCGAGCTGAGTTGTGATGATCATCATCATCTGCTGCT 136
QY 559 GGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 618
DB 137 GGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 196
QY 619 ACGGTCTTCAATCAAGCCGCGCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 678
DB 197 ACGGTCTTCAATCAAGCCGCGCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 256
QY 679 AGATGCTGTGAGGCTTGTGAGAGACAGTGTGAGAGACAGTGTGAGAGACAGTGTGAGAG 738
DB 257 AGATGCTGTGAGGCTTGTGAGAGACAGTGTGAGAGACAGTGTGAGAGACAGTGTGAGAG 316
QY 739 CTAAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 798
DB 317 CTAAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 376
QY 799 CTTCCAGCGCTTCCAGCCCACTTACCGTACCTGACAGCAGATGACCTTGCACCCAC 858
DB 377 CTTCCAGCGCTTCCAGCCCACTTACCGTACCTGACAGCAGATGACCTTGCACCCAC 436
QY 859 CATCTCGCTGTGACAGCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 918
DB 437 CATCTCGCTGTGACAGCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 496
QY 919 TCGGAGACCCCGAGCAGCAGCTGAACTGAACTGAACTGAACTGAACTGAACTGAACTG 978
DB 497 TCGGAGACCCCGAGCAGCAGCTGAACTGAACTGAACTGAACTGAACTGAACTGAACTG 556
QY 979 AACCATCTTCCAGCAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGA 1038
DB 557 AACCATCTTCCAGCAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGA 616
QY 1039 CAGTAATCTGAGGATCAAGGCGCACTGTAAGCGAGCGGCGGCGGCGGCGGCGGCGG 1098
DB 617 CAGTAATCTGAGGATCAAGGCGCACTGTAAGCGAGCGGCGGCGGCGGCGGCGGCGGCGG 676
QY 1099 GCGGACCTTCAAGCAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGA 1158
DB 677 GCGGACCTTCAAGCAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGA 736
QY 1159 CAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1218
DB 737 CAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 796
QY 1219 AGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1278
DB 797 AGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 856
QY 1279 TCCCGAGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1321
DB 857 TCCCGAGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 899

RESULT 13

US-11-051-454-412
Sequence 412, Application US/11051454
Publication No. US20050191673A1

GENERAL INFORMATION:

APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Endesig, Wilson O.
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gorbacheva, Bella
APPLICANT: Hoersch, Sebastian
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Monney, Angela M.

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2006, 09:34:50 ; Search time 1731.47 Seconds
(without alignments)
1626.862 Million cell updates/sec

Title: US-09-934-249-1

Perfect score: 1321
Sequence: 1 cgaccgcgctctcgagcgcga.....ctgcgtagtgtaaacgcag 1321

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7209121 seqs, 1066183437 residues

Total number of hits satisfying chosen parameters: 14418242

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA.New:*
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2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq1:*
7: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq1:*
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9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
12: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq4:*
13: /cgn2_6/ptodata/2/pubpna/US66_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	802.2	60.7	1141	12	US-11-186-284-208
2	128	9.7	129	8	US-10-310-914A-7163
3	97	7.3	97	8	US-10-310-914A-6542
4	95.4	7.2	97	8	US-10-310-914A-1107
5	87.6	6.6	94	8	US-10-310-914A-1106
6	69.2	5.2	16917	12	US-11-124-367A-5000
7	68.8	5.2	16917	12	US-11-124-367A-5000
8	68.2	5.2	2600	6	US-09-925-065A-92367
9	67	5.1	1608	6	US-09-925-065A-37513
10	67	5.1	1608	6	US-09-925-065A-37514
11	67	5.1	1608	6	US-09-925-065A-37515
12	67	5.1	2600	6	US-09-925-065A-92368
13	67	5.1	3240	12	US-11-052-554A-529
14	65.8	5.0	2136	12	US-11-052-554A-539
15	65.6	5.0	191684	12	US-11-121-086-2
16	65.4	5.0	2562	12	US-11-052-554A-533
17	63.6	4.8	191684	12	US-11-121-086-2
18	63.4	4.8	23187	9	US-11-236-198-1
19	63	4.8	1966	7	US-10-506-766-1
20	63	4.8	2584	8	US-10-821-234-836

21	62.8	4.8	2072	12	US-11-136-527-2747	Sequence 2747, App
22	61.6	4.7	2954	8	US-11-241-347-2	Sequence 2, Appl1
23	61.6	4.7	18138	8	US-10-995-561-13385	Sequence 13385, A
24	61.4	4.6	18163	8	US-10-310-914A-7162	Sequence 7162, App
25	61.4	4.6	2250	12	US-11-052-554A-532	Sequence 532, App
26	61.2	4.6	26688	8	US-10-933-025-42	Sequence 22, Appl1
27	61	4.6	153376	12	US-11-121-086-5	Sequence 5, Appl1
28	61	4.6	172543	12	US-11-121-086-6	Sequence 6, Appl1
29	60.8	4.6	2825	12	US-11-136-527-192	Sequence 192, App
30	60.4	4.6	2514	12	US-11-052-554A-543	Sequence 543, App
31	60.2	4.6	1609	6	US-09-925-065A-9327	Sequence 9327, App
32	60.2	4.6	1609	6	US-09-925-065A-9328	Sequence 9328, App
33	60	4.5	170995	12	US-11-121-086-35	Sequence 35, Appl1
34	59.8	4.5	3167	6	US-09-925-065A-21764	Sequence 21764, A
35	59.6	4.5	4739	8	US-10-770-726-2	Sequence 2, Appl1
36	59.4	4.5	3234	12	US-11-121-438-9	Sequence 9, Appl1
37	59.4	4.5	10968	12	US-11-075-185-35	Sequence 35, Appl1
38	59.4	4.5	78869	12	US-11-075-185-1	Sequence 1, Appl1
39	59.4	4.5	165857	12	US-11-121-086-34	Sequence 34, Appl1
40	59.2	4.5	9406	12	US-11-136-527-748	Sequence 748, App
41	59.2	4.5	16917	12	US-11-124-367A-5000	Sequence 5000, App
42	59	4.5	1609	6	US-09-925-065A-9329	Sequence 9329, App
43	59	4.5	12277	6	US-10-477-507A-3	Sequence 3, Appl1
44	58.8	4.5	2406	12	US-11-052-554A-550	Sequence 550, App
45	58.2	4.4	3081	8	US-10-514-863-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-11-186-284-208
Sequence 208, Application US/11186284
Publication No. US20050266493A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kametkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILE REFERENCE: MP001-029P2RNM
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 208
LENGTH: 1141
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (96) ... (854)
US-11-186-284-208
Query Match 60.7%; Score 802.2; DB 12; Length 1141;
Best Local Similarity 98.4%; Pred. No. 4,5e-160;
Matches 810; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
499 TTGTTCCAGCAGATGAGATCATCGAGTGTGTTGTTGATCATCATCATCGTGT 558


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LOCATION: 1671, 1672, 1673, 1674, 1675, 1676, 1677, 1678, 1679, 1680,
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LOCATION: 1691, 1692, 1693, 1694, 1695, 1696, 1697, 1698, 1699,
OTHER INFORMATION: n = A,T,C or G
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1700, 1701, 1702, 1703, 1704, 1705, 1706, 1707, 1708, 1709,
LOCATION: 1710, 1711, 1712, 1713, 1714, 1715, 1716, 1717, 1718, 1719,
LOCATION: 1720, 1721, 1722, 1723, 1724, 1725, 1726, 1727, 1728, 1729,
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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OTHER INFORMATION: n = A,T,C or G
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1817, 1818, 1819, 1820, 1821, 1822, 1823, 1824, 1825, 1826,
LOCATION: 1827, 1828, 1829, 1830, 1831, 1832, 1833, 1834, 1835, 1836,
LOCATION: 1837, 1838, 1839, 1840, 1841, 1842, 1843, 1844, 1845, 1846,
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OTHER INFORMATION: n = A,T,C or G
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1856, 1857, 1858, 1859, 1860, 1861, 1862, 1863, 1864, 1865,
LOCATION: 1866, 1867, 1868, 1869, 1870, 1871, 1872, 1873, 1874, 1875,
LOCATION: 1876, 1877, 1878, 1879, 1880, 1881, 1882, 1883, 1884, 1885,
LOCATION: 1886, 1887, 1888, 1889, 1890, 1891, 1892, 1893, 1894
OTHER INFORMATION: n = A,T,C or G
US-11-124-367A-5000

Query Match      5.2%; Score 69.2; DB 12; Length 16917;
Best Local Similarity 50.0%; Pred. No. 9, 7e-06;
Matches 199; Conservative 0; Mismatches 198; Indels 1; Gaps 1;

QY 60 GCGCGCGCGCGCGCGCGCGAGCGCGCTCGCGGGAGAACTGAGCGGACAGGCTCAGCCCC 119
DB 11659 GCTGAGGCGGCGGCTGCGCGCGTGCAGCGCTGAGGCGGCGGACGCGAGAGACTGTGAGA 116000
QY 120 CCGCGGCGAGCGCGCGCGCGCTGCGCGCGCAGCCATTTCGCGACCGCCACCGCGGGGACTGCC 179
DB 11599 GAGCGGCGGAGCGACCGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 115400
QY 180 GAGGCGCGCGGCGGCTGCGAGGCGGAGCGCGGCGGCGCGGCGGCGGCGGCGGCGGCGGCG 239
DB 11539 ACCCGGCGGCGGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 114800
QY 240 CTGAGCGCGCGCGCGCGCGCGCGGGAATCTGCGCGGACCGCGAGCGCGCGGAGCGCGGCGG 299
DB 11479 CTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 114200
QY 300 CTTCCCGCGCGCGCGCGCGCTTCTGCGATGCGGAGCGCCCAAGCTCCGGGCGCGCGCGGAGGCC 359
DB 11419 GCTGCGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 113600
QY 360 CCGCGCGCGCGCGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 418
DB 11359 CCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 113000
QY 419 CGCTTGATGGGGGTCAACAGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 456
DB 11299 GGGCGGCGCGGGGGGAACTGTCTCGCGCGCGCGAGCCCC 11262

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RESULT 7
US-11-052-554A-529
; Sequence 529, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; FILE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 529
; LENGTH: 3240
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-529

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Query Match	5.2%;	Score 68.8;	DB 12;	Length 3240;
Best Local Similarity	49.8%;	Pred. No. 1.2e-05;		
Matches 229;	Conservative	0;	Mismatches 227;	Indels 4;
				Gaps 2

QY	2	AACCGCGGCTCGAGAGCGAAACCCATCTCTTGGACTTGAATGAGAGAGAGAGCGCG	61
Db	1069	GCCGCGCGCAACGCGCGCACCGGCGCAGAGGCGCGACTGTGTGGCCGCGCGACCGT	1128
QY	62	GCGCGCGCGCGCGCGGAGCGCTCGCTGGGTGGGAAAGCTAAGCGCAGAGCTCAGCCCC	121
Db	1129	ATCGGTGGGTGCTCGGCGCGCGCGCAAGGGCGGCAACCGCGCGGACCGGGAAGTGGCGTGGC	1188
QY	122	GCGCGAGCGCGCGCGCCCGCTGCGACGCCATTTCCGGAAGCAGCCGCGGCGACTGGCGG	180
Db	1189	GCGCGCGCGCGCGCGCGCGCGCGCAACACAGTCCCGGCGCAACGGCGCGAGAGT	1248
QY	181	-ACGCCCCCGGGCTTGCACAGGGAGAGCGCGGGGGCGCAGCGAGCGGTCCCGCA	239
Db	1249	CAGGCGGCGAGGAGGTGTGTGCGGTGGGCGCGCGGGGCTGTGCGGCGCGGTGGCGGCT	1308
QY	240	CTGAGACCCCGCGCGCGCCCCGGGAACTTTGGCGCGACCGAGCCCCGAGCGGGCGCG	299
Db	1309	AACGGAACCGCTGGCAACCGGCGCGCAAGCGGTGTGCGCGGACCGCGCGCGCGCGCA	1368
QY	300	CGTCCCCCGCGCGCGCTCTGTGACATGCGGGGCCACAGCTCCGAGCGCGCGCGAGCC	359
Db	1369	GCTCTCTCAGCTACACACGCGCGGCGCAGCGGCGGCGCGG--CGGCAACGAGGCGACGGG	1428
QY	360	CCCCCGCGCGCCCGGAGCCCCCGCGCGCCCGCGCGCGCGCGCGCGCTCTCATGACC	419
Db	1427	GAGCGCGCGCGCGCGCGCGCACCGGAGCGCGCGCGCACCGCGGCGCGCGCGACG	1488
QY	420	GCTTGAATGGGGGTCAACAGACCGCGCGCGCGCGCGCGG	459
Db	1487	GCGAGACAAGTGGCGAGGCGGCGCGCGCGCGGTGCCG	1526

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RESULT 8
US-09-925-065A-92367/c
; Sequence 92367, Application US/09925065A
; Publication No. US20040181048A1
;
GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243, 096

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1 PRIOR FILING DATE: 2000-10-24
2 PRIOR APPLICATION NUMBER: US 60/252,147
3 PRIOR FILING DATE: 2000-11-20
4 PRIOR APPLICATION NUMBER: US 60/250,092
5 PRIOR FILING DATE: 2000-11-30
6 PRIOR APPLICATION NUMBER: US 60/261,766
7 PRIOR FILING DATE: 2001-01-16
8 PRIOR APPLICATION NUMBER: US 60/269,846
9 PRIOR FILING DATE: 2001-05-09
10 NUMBER OF SEQ ID NOS: 957086
11 SOFTWARE: FASTSQ for Windows Version 4.0
12 SEQ ID NO 92367
13 LENGTH: 2600
14 TYPE: DNA
15 ORGANISM: Homo sapiens
16 FEATURE:
17 NAME/KEY: misc_feature
18 LOCATION: (1)..(2600)
19 OTHER INFORMATION: n = A,T,C or G
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21 US-09-925-065A-92367

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Query Match	5.2%	Score 68.2	DB 6	Length 2600
Best Local Similarity	49.6%	Pred. No. 1.6e-05		
Matches 200; Conservative	1	Mismatches 199	Indels 3	Gaps 1

QY 59 GCGCGCGCGCGCGCGCGCGAGAGCGCTCGGCTCGGGGAAAGCTTAAGCGCGAGAGGCTCAACG 118

Db 1422 GCTTCGCGCGCGCTCGCGGGGAGAGACGGTTCTCGGGGAGACCGCGCCGACACTGCGCGCGCG 1363

QY 119 CGCGCGGAGCGCGCGCGCCCGCGCTGCGACGCAATTTTCGAGCGCCACCCGCGGGGCACTGC 178

Db 1362 GCGGTGCGTGGGGGAGAGCCGCGAGGATCGCCGAGGGACGGTCTGCGCGCGCCCGCGGGTGC 1303

QY 179 CGACGCGCCCGCGGCGCTGCGCGAGGAGAGCGCCGCGGGGGGCGAGCGGAGCGCGCTCCCGGCG 238

Db 1302 CGGTGTCGCGCGCGCGCGGTGAGGCCCGCCGCGGTGTGTCGCGCGCGCGGTTCGCGCGCTC 1243

QY 239 ACTGAGCGCCCGCGCGCGCGCCCGGAGAACTTGGCGGCGACCCGAGGCCGCGGAGCGCGGGGCGC 298

Db 1242 GAGGGGATCCCGTGGCGTCCCTTCGCCGCGGCGCGCTTTCGTGCGGCTTTCGCCGTGC 1183

QY 299 GCGTTCGCCGCGCGCGCGCTCTCGT---CATGCGGGGCGCCAGCTTCGAGGCGCGGCGCGGA 355

Db 1182 CCGGCGCTCGCGCGTGTCTCTCGTCTTCTCCCGGCGCGCTTTCGAAACGGGATCGGG 1122

QY 356 GCGCGCCCGCGCGCGCCCGAGACCCCGCGCGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCTTCATG 415

Db 1122 CGTCCCGCGGGGCGCTTCGCTTCCCGGAGCTGCGCGGCGCGCCCTTCCCGAGGCGTCCGTC 1063

QY 416 CACCGCTTGAATGGGGGTCAACGACGCGCGCGCGCGCGCGCGCG 458

Db 1062 CGGGCGTTCGCGCTCGGGGAGAGCCCGTCTTCCCGCGTGGCG 1020

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RESULT 9
US-09-925-065A-37513/C
; Sequence 37513, Application US/09925065A
; Publication No. US20040181048A1
;
GENERAL INFORMATION:
;
APPLICANT: Wang, David G.
;
TITLE OF INVENTION: Identification and Mapping of Single
;
FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
;
FILE REFERENCE: 108827.135
;
CURRENT APPLICATION NUMBER: US/09/925, 065A
;
CURRENT FILING DATE: 2001-08-08
;
PRIOR APPLICATION NUMBER: US 60/243, 096
;
PRIOR FILING DATE: 2000-10-24
;
PRIOR APPLICATION NUMBER: US 60/252, 147
;
PRIOR FILING DATE: 2000-11-20
;
PRIOR APPLICATION NUMBER: US 60/250, 092
;
PRIOR FILING DATE: 2000-11-30
;
PRIOR APPLICATION NUMBER: US 60/261, 766
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PRIOR FILING DATE: 2001-01-16
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